

STIC-Biotech/ChemLib

164232

From: Whiteman, Brian
Sent: Monday, August 29, 2005 4:04 PM
To: STIC-Biotech/ChemLib
Subject: seq search

09/801,371

SEQ ID NO: 1 and 2

1) the commercial databases, and the issued and published US application databases

Thank you,

Brian Whiteman
Remsen, 2D14
mail box 2C18
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 9/1/05
Date Completed: 9/1/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: 2 AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 0311
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:55:28 ; Search time 1896.05 Seconds
(without alignments)
2657.805 Million cell updates/sec

Title: US-09-801-371A-1
Perfect score: 104
Sequence: 1 gaattcaaacctggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
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- 8: gb_pl:*
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- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	104	100.0	400	11	G13533	G13533 SHGC-11076
2	104	100.0	787	6	BD137681	BD137681 Self-regu
3	104	100.0	787	6	AR300453	AR300453 Sequence
4	104	100.0	787	6	BD070551	BD070551 Self-regu
5	104	100.0	1275	6	I08430	I08430 Sequence 5
6	104	100.0	1323	6	I07953	I07953 Sequence 6
7	104	100.0	1324	6	E00702	E00702 cDNA encodi
8	104	100.0	1324	6	I03610	I03610 Sequence 2
9	104	100.0	1465	6	I04244	I04244 Sequence 2
10	104	100.0	1585	6	A37272	A37272 Sequence 12
11	104	100.0	1585	6	I04169	I04169 Sequence 1
12	104	100.0	1585	6	I04198	I04198 Sequence 1
13	104	100.0	1585	6	I08384	I08384 Sequence 5
14	104	100.0	1585	6	I08429	I08429 Sequence 3
15	104	100.0	1585	6	AR380784	AR380784 Sequence
16	104	100.0	1585	9	HUMTNFAA	M10988 Human tumor
17	104	100.0	1606	6	I07541	I07541 Sequence 22
18	104	100.0	1643	6	AR146199	AR146199 Sequence
19	104	100.0	1643	6	AR366225	AR366225 Sequence

20	104	100.0	1643	9	HSTNFR	X01394 Human mRNA
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25	104	100.0	2570	6	AR300460	AR300460 Sequence
26	104	100.0	3103	9	HUMTNFX	M26331 Human tumor
27	104	100.0	3634	6	AR100270	AR100270 Sequence
28	104	100.0	3634	6	AR149925	AR149925 Sequence
29	104	100.0	3634	6	BD227798	BD227798 Antisense
30	104	100.0	3634	6	BD271232	BD271232 Predictio
31	104	100.0	3634	6	BD064008	BD064008 Novel exp
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34	104	100.0	6974	9	AB088112	AB088112 Homo sapi
35	104	100.0	7112	6	AX100950	AX100950 Sequence
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C 39	104	100.0	10728	6	AR562497	AR562497 Sequence
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ALIGNMENTS

RESULT 1
G13533
LOCUS G13533 SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION G13533
ACCESSION G13533
VERSION G13533.1 GI:1129272
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: CACTAAGAAATTCAAACTGGGGC
Primer B: GAGGAAGGCCTAAGGTCCAC
STS size: 166
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from M10988 -- Unigene.

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STS
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Db 216 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 275
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QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
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RESULT 2
BD137681
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Tatake,R.J., Marlin,S.D. and Barton,R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: JP 2002504381-A 7 12-FEB-2002;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002504381-A/7
PD 12-FEB-2002
PF 12-JAN-1999 JP 20005333579
PR 27-FEB-1998 US 60/076316
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
C12N15/09,A61K31/7088,A61K48/00,A61P1/04,A61P3/10,A61P17/06, PC
A61P25/00,
PC A61P29/00,A61P43/00,C12N9/64,C12Q1/68//C12N5/10,C12N15/00, PC
C12N5/00
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Location/Qualifiers
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FEATURES
source
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
AR300453
Sequence 7 from patent US 6537784.
AR300453
AR300453.1 GI:31687895
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 787)
Tatake,R.J., Marlin,S.D. and Barton,R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: US 6537784-A 7 25-MAR-2003;
Location/Qualifiers
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RESULT 4
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BD070551
Self-regulated apoptosis of inflammatory cells by gene therapy.
BD070551
BD070551.1 GI:22616154
JP 2001516210-A/13.
unidentified
unidentified
unclassified.
1 (bases 1 to 787)
Tatake,R.J., Marlin,S.D. and Barton,R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: JP 2001516210-A 13 25-SEP-2001;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
OS Unidentified
PN JP 2001516210-A/13
PD 25-SEP-2001
PF 27-FEB-1998 JP 1998537909
PR 28-FEB-1997 US 60/039266
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
A61K31/70,C07H21/04,C12N15/12,C12P19/34
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CC Topology: Linear;
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DEFINITION									
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I08430									
VERSION									
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Unknown.									
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REFERENCE									
1 (bases 1 to 1275)									
AUTHORS									
Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.									
TITLE									
CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR									
JOURNAL									
NECROSIS FACTOR PROTEINS									
Patent: WO 8604606-A 5 14-AUG-1986;									
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VERSION									
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1 (bases 1 to 1323)									
AUTHORS									
Aggarwal,B.B., Lee,S.H., Goeddel,D.V. and Nedwin,G.E.									
TITLE									
Tumor necrosis factor, methods for its preparation, compositions									
containing it, DNA encoding it and assay method using such DNA									
JOURNAL									
Patent: EP 0168214-A2 6 15-JAN-1986;									
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RESULT 8
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DEFINITION Sequence 2 from Patent US 4650674.
ACCESSION I03610
VERSION I03610.1 GI:268632
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1324)
AUTHORS Aggarwal,B.B. and Lee,S.He.
TITLE Synergistic cytotoxic composition
JOURNAL Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco, CA
FEATURES
source 1. .1324
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QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 854
RESULT 9
I04244
LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4677197.
ACCESSION I04244
VERSION I04244.1 GI:268725
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1465)
AUTHORS Lin,L.S. and Yamamoto,R.
TITLE Purification method for tumor necrosis factor
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
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A37272
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9404196.

ACCESSION A37272
VERSION A37272.1 GI:2294369
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1585)
AUTHORS Vile,R.G. and Hart,I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
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LOCUS I04169 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677063.
ACCESSION I04169
VERSION I04169.1 GI:268716
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
Arsdell,J.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677063-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
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LOCUS I04198 1585 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4677064.
ACCESSION I04198
VERSION I04198.1 GI:268719
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Van Arsdel, J.N.
TITLE Human tumor necrosis factor
JOURNAL Patent: US 4677064-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
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LOCUS I08384 1585 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 5 from Patent WO 8602381.
ACCESSION I08384
VERSION I08384.1 GI:588904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
Arsdel, J.N.
TITLE HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8602381-A 5 24-APR-1986;
FEATURES Location/Qualifiers
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LOCUS I08429 1585 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 8604606.
ACCESSION I08429
VERSION I08429.1 GI:588859
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)

AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 3 14-AUG-1986;
FEATURES Location/Qualifiers
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Db 1063 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106
RESULT 15
AR380784
LOCUS AR380784 1585 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1329 from patent US 6607879.
ACCESSION AR380784
VERSION AR380784.1 GI:40088418
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological
response gene expression
JOURNAL Patent: US 6607879-A 1329 19-AUG-2003;
FEATURES Location/Qualifiers
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	104	100.0	787	2	AAZ20979	Aaz20979 Human TNF
3	104	100.0	792	13	ADR12297	Adr12297 Human tum
4	104	100.0	1275	1	AAN60558	Aan60558 Sequence
5	104	100.0	1323	1	AAN60363	Aan60363 Sequence
6	104	100.0	1324	3	AAA34963	Aaa34963 Human ade
7	104	100.0	1324	3	AAF21085	Aaf21085 Human low
8	104	100.0	1324	10	ABZ96779	Abz96779 Human nuc
9	104	100.0	1324	11	ABD20628	Abd20628 Human pul
10	104	100.0	1560	1	AAN80219	Aan80219 Sequence
11	104	100.0	1581	12	ADQ83817	Adq83817 Human tum
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13	104	100.0	1585	8	ACA64836	Aca64836 Human TNF
14	104	100.0	1585	10	ADF76346	Adf76346 Novel hum
15	104	100.0	1585	11	ADI32003	Adi32003 Human CDN
16	104	100.0	1585	12	ADO19587	Ado19587 Human PRO
17	104	100.0	1585	13	ADR24640	Adr24640 Breast ca
18	104	100.0	1585	13	ADP54654	Adp54654 Human PRO
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24	104	100.0	1643	8	AAD49644	Aad49644 Human tum
25	104	100.0	1643	10	ADC35185	Adc35185 Human CDN
26	104	100.0	1643	10	AAD63904	Aad63904 Human TNF
27	104	100.0	1643	10	ACC57575	Acc57575 Polynucle
28	104	100.0	1643	13	ADR26040	Adr26040 Breast ca
29	104	100.0	1650	8	ACF64375	Acf64375 Human TNF
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35	104	100.0	3634	2	AAV39005	Aav39005 TNF-alpha
36	104	100.0	3634	2	AAAX09014	Aax09014 Tumour ne
37	104	100.0	3634	3	AAA40760	Aaa40760 Human tum
38	104	100.0	3634	3	AAC63770	Aac63770 Human TNF
39	104	100.0	3634	8	ACC57891	Acc57891 Human tum
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42	104	100.0	3634	10	ACF63382	ACf63382 Human TNF
43	104	100.0	3634	12	ADQ29070	Adq29070 Human tum
44	104	100.0	3634	13	ADR02586	Adr02586 Human tum
45	104	100.0	4830	12	ACF57523	ACf57523 Human TNF

ALIGNMENTS

RESULT 1
AAZ99816
ID AAZ99816 standard; RNA; 104 BP.
XX
AC AAZ99816;
XX

DT 12-JUL-2000 (first entry)
XX

DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX

KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; es.
XX

OS Homo sapiens.
XX

PN WO200014255-A1.
XX

PD 16-MAR-2000.
XX

PF 06-SEP-1999; 99WO-IL000483.
XX

PR 07-SEP-1998; 98IL-00126112.
XX

PA (YISS) YISSUM RES & DEV CO.
XX

PI Kaempfer R, Osman F, Jarroux N, Ben-Asouli Y;
XX

DR WPI; 2000-257000/22.
XX

PT Regulation of gene expression by mRNA splicing is carried out using a cis
PT -acting nucleotide sequence controlled by phosphorylation of the alpha-
PT subunit of eukaryotic initiation factor 2.
XX

PS Claim 4; Page 15; 75pp; English.
XX

CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a gene
CC which harbours at least one cis-acting nucleotide sequence. This removal
CC is effected during the production of mRNA of the gene, and depends on
CC activation of a trans-acting factor which is an RNA-activated protein
CC kinase capable of phosphorylating the alpha-subunit of eukaryotic

CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can be
CC used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention
XX
SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.1e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTTGCCCGAGAAATGCTGC 104
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RESULT 2
AAZ20979
ID AAZ20979 standard; DNA; 787 BP.
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AC AAZ20979;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human TNFalpha 3'UTR.
XX
KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus; diabetes;
KW ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
PN WO9943840-A1.
XX
PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99WO-US0000637.
XX
PR 27-FEB-1998; 98US-0076316P.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Tataka RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX
PT A chimeric polynucleotide consisting of a tissue necrosis factor (TNF)
PT promoter and an apoptosis-inducing Granzyme B polynucleotide.
XX
PS Example 1; Page 60-61; 71pp; English.
XX
CC This sequence represents a human TNFalpha (tumour necrosis factor alpha)
CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were
CC constructed comprising at least one TNFalpha promoter enhancer region
CC (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA encoding
CC the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha
CC 3'UTR sequence. TNFalpha is one of a number of cytokines produced by
CC inflammatory cells. Upregulation and/or dysregulation of cytokines in
CC inflamed tissue may be directly or indirectly responsible for
CC exacerbation of chronic inflammatory diseases. Introduction of the
CC chimeric nucleotide to activated inflammatory cells causes them to

CC undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide
CC may be useful for treating inflammatory disorders such as multiple
CC sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus
CC host disease, lupus erythematosus, insulin-dependent (type I) diabetes
CC mellitus, ankylosing spondylitis, and in particular, rheumatoid
CC arthritis. The use of such chimeric nucleotides offers simpler and
CC cheaper long-term relief, in comparison with existing conventional
CC pharmaceutical and invasive surgery methods
XX
SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 222 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281
|||||
QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTTGCCCGAGAAATGCTGC 104
|||||
Db 282 GAATCTGGAGACCCAGGAGCCTTTGGTTCTTGCCCGAGAAATGCTGC 325
|||||

RESULT 3
ADRI12297
ID ADRI12297 standard; DNA; 792 BP.
XX
AC ADRI12297;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human tumour necrosis factor alpha 3'-untranslated region DNA.
XX
KW ss; cytostatic; VEGF modulator; angiogenesis inhibitor;
KW UTR-dependent expression; vascular endothelial growth factor;
KW untranslated region; cancer; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO2004065561-A2.
XX
PD 05-AUG-2004.
XX
PF 21-JAN-2004; 2004WO-US001643.
XX
PR 21-JAN-2003; 2003US-0441637P.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Cao L, Trifillis P;
XX
DR WPI; 2004-571681/55.
XX
PT Identifying modulators of untranslated region-dependent expression of a
PT VEGF gene, useful for treating cancer, comprises contacting a compound
PT with a cell or translation mixture containing a reporter gene linked to a
PT VEGF gene UTR.
XX
PS Example; SEQ ID NO 6; 251pp; English.
XX
CC A method of identifying (M1) a compound that modulates untranslated
CC region-dependent expression of a vascular endothelial growth factor
CC (VEGF) gene comprises contacting a member of a library of compounds with
CC a cell or cell-free translation mixture containing a reporter gene
CC operably linked to an untranslated region (UTR) of the VEGF gene, and
CC detecting expression of the reporter gene. A compound is identified as
CC modulator if the level of expression of the reporter gene in the presence
CC of the compound is altered as compared to that in the absence of the
CC compound or in the presence of a control. Compounds identified by M1 are
CC useful for treating, preventing or ameliorating cancer or its symptoms,
CC and/or for inhibiting angiogenesis. This sequence corresponds to a
CC therapeutic untranslated region used in the invention.

```

XX      Sequence 792 BP; 192 A; 203 C; 172 G; 225 T; 0 U; 0 Other;
SQ
    Query Match      100.0%; Score 104; DB 13; Length 792;
    Best Local Similarity 100.0%; Pred. No. 5.4e-25;
    Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      219 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 278

QY      61 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      279 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 322

RESULT 4
AAN60558
ID      AAN60558 standard; DNA; 1275 BP.
XX
AC      AAN60558;
XX
DT      28-JUL-1991 (first entry)
XX
DE      Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser
DE      69 in pAW731.
XX
KW      Antitumour; anticancer; ss.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..474
FT      FT      /*tag= a
XX
XX      WO8604606-A.
PN
XX
PD      14-AUG-1986.
XX
PF      03-FEB-1986; 86WO-US000236.
XX
PR      07-FEB-1985; 85US-00698939.
XX
PA      (CETU ) CETUS CORP.
XX
PI      Mark DF, Lin LS, Lu SDY, Wang AM;
XX
DR      WPI; 1986-225458/34.
DR      P-PSDB; AAP60656.
XX
PT      New synthetic muteins of human tumour necrosis factor protein - are obtd.
PT      by direct mutagenesis and retain antitumour activity.
XX
PS      Disclosure; Fig 3a; 47pp; English.
XX
CC      The sequence encoding TNF produced by the promyelocytic leukemia cell
CC      line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see
CC      AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
CC      sequence appears to be involved in disulphide linkages. The patentors
CC      claim a novel synthetic mutein of a biologically active hTNF protein,
CC      having at least one cysteine residue free from a disulphide link and non-
CC      essential to the activity and having at least one of the cysteine
CC      residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
CC      claimed
XX
SQ      Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;

    Query Match      100.0%; Score 104; DB 1; Length 1275;
    Best Local Similarity 100.0%; Pred. No. 6.2e-25;
    Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      693 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 752

QY      61 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      753 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 796

RESULT 5
AAN60363
ID      AAN60363 standard; DNA; 1323 BP.
XX
AC      AAN60363;
XX
DT      19-JUN-1991 (first entry)
XX
DE      Sequence encoding human tumour necrosis factor.
XX      hTNF; tumour; cancer; interferon; ds.
XX
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      1..534
FT      FT      /*tag= a
FT      sig_peptide 1..60
FT      FT      /*tag= b
FT      FT      /label= Secretory leader peptide
FT      mat_peptide 61..534
FT      FT      /*tag= c
XX
PN      EP168214-A.
XX
PD      15-JAN-1986.
XX
PF      03-JUL-1985; 85EP-00304758.
XX
PR      05-JUL-1984; 84US-00627959.
PR      05-JUL-1984; 84US-00628059.
PR      05-JUL-1984; 84US-00628060.
PR      03-DEC-1984; 84US-00677156.
PR      03-DEC-1984; 84US-00677257.
PR      03-DEC-1984; 84US-00677267.
PR      03-DEC-1984; 84US-00677454.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;
XX
DR      WPI; 1986-015483/03.
DR      P-PSDB; AAP60417.
XX
PT      Pure tumour necrosis factor and mutant forms - new DNA coding sequences
PT      and transformed cells.
XX
PS      Claim 20; Fig 10; 90pp; English.
XX
CC      Sequence encodes the pure human tumour necrosis factor, mutants of which
CC      are covered by the claims. TNF and mutants are useful in treating
CC      tumours, especially in tandem with interferon. The encoding sequence may
CC      be used to create plasmid pTrpXAPTNF, allowing transformation of an
CC      E.coli host for the expression of TNF
XX
SQ      Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;

    Query Match      100.0%; Score 104; DB 1; Length 1323;
    Best Local Similarity 100.0%; Pred. No. 6.2e-25;
    Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      750 GAATTCAAACCTGGGCGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 809

QY      61 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
```

Db 810 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 853
|||||
AA34963
ID AAA34963 standard; DNA; 1324 BP.
XX
AC AA34963;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 814-815; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 3; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGCTCCAGAACTCACTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 751 GAATTCAAACTGGGCTCCAGAACTCACTACAGCTTTGATCCCTGACATCTG 810
|||||
QY 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 811 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 854
|||||
RESULT 7
AAF21085
ID AAF21085 standard; DNA; 1324 BP.
XX
AC AAF21085;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2652.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 887; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide

transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 3; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 854

RESULT 8
ABZ96779

ID ABZ96779 standard; DNA; 1324 BP.

AC ABZ96779;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human nucleic acid sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.

XX

OS Homo sapiens.

XX

PN WO200285308-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013135.

XX

PR 24-APR-2001; 2001US-0286137P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-229219/22.

XX

PT Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

XX

PS Disclosure; SEQ ID NO 12021; 872pp; English.

XX

CC The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the

initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 10; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 854

RESULT 9
ABD20628

ID ABD20628 standard; DNA; 1324 BP.

XX

AC ABD20628;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human pulmonary and inflammatory target DNA #239.

XX

KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallergic; antiinflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds.

XX

OS Homo sapiens.

XX

PN WO200285309-A2.

XX

PD 31-OCT-2002.

XX

PF 23-APR-2002; 2002WO-US013143.

XX

PR 24-APR-2001; 2001US-0286036P.

XX

PA (EPIG-) EPIGENESIS PHARM INC.

XX

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX

DR WPI; 2003-093058/08.

XX

PT Pharmaceutical composition for treating asthma, has antisense oligonucleotide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX Claim 15; SEQ ID NO 12021; 763pp; English.

PS

XX This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it

XX

SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 11; Length 1324;
Best Local Similarity 100.0%; Pred. No. 6.2e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
751 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810

QY 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104

Db 811 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 854

RESULT 10
AAN80219

ID AAN80219 standard; DNA; 1560 BP.

XX AAN80219;

XX

DT 28-DEC-1990 (first entry)

XX

DE Sequence of pE4 encoding human tumour necrosis factor (TNF).

XX

KW Lymphokine; antitumour; ss.

XX Homo sapiens.

OS

XX

FH Key Location/Qualifiers

FT CDS 86..313

FT /*tag= a

FT mat_peptide 314..787

FT /*tag= b

XX

XX WO8806625-A.

PN

XX

PD 07-SEP-1988.

XX 25-JAN-1988; 88WO-US000183.

PF

XX 26-FEB-1987; 87US-00019221.

PR

XX (CETU) CETUS CORP.

PA

XX Mark DF, Lin LS, Thomson JW, Yamamoto R;

PI

XX WPI; 1988-271165/38.

DR

DR P-PSDB; AAP80728.

XX

PT Human tumour necrosis factor muteins - having comparable biological activity with improved stability and ease of purification.

PT

XX Disclosure; Fig 1-1 to 1-2; 5lpp; English.

PS

XX A human TNF protein which is modified from the sequence shown in AAP80728, including naturally occurring allelic variants is claimed. Also claimed are: recombinant DNA sequences encoding the protein (AAN80219) and control sequences for expression; a vector; a transformed host cell; a method of producing the protein by culturing the host cell;

CC pharmaceutical compsn. of the protein and a carrier and a method of treating tumour burden with the compsn. The muteins are capable of the range of biological activities exhibited by native TNF but exhibit improved stability and ease of purification

CC

XX Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 104; DB 1; Length 1560;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
1003 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

Db

QY 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104

Db 1063 GAATCTGGAGACCAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1106

RESULT 11
ADQ83817

ID ADQ83817 standard; cDNA; 1581 BP.

XX ADQ83817;

AC

XX 07-OCT-2004 (first entry)

DT

XX

DE Human tumour-associated antigenic target (TAT) cDNA sequence #631.

XX

KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.

KW

XX Homo sapiens.

OS

XX WO2004060270-A2.

PN

XX 22-JUL-2004.

PD

XX

PF 15-OCT-2003; 2003WO-US029126.

XX

PR 18-OCT-2002; 2002US-0418988P.

XX

PA (GETH) GENENTECH INC.

PA (WUTD/) WU T D.

PA (ZHOU/) ZHOU Y.

XX

PI Wu TD, Zhou Y;

XX

DR WPI; 2004-534300/51.

XX

PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 631; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 1581 BP; 351 A; 471 C; 385 G; 374 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 12; Length 1581;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 999 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1058
QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
Db 1059 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1102

RESULT 12
AAN60557
ID AAN60557 standard; DNA; 1585 BP.
XX
AC AAN60557;
XX
DT 28-JUL-1991 (first entry)
XX
DE Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.
XX
KW Antitumour; anticancer; ss.
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 86..313
FT mat_peptide /*tag= a
FT 314..787
FT /*tag= b
XX
PN WO8604606-A.
XX
PD 14-AUG-1986.
XX
PF 03-FEB-1986; 86WO-US000236.
XX
PR 07-FEB-1985; 85US-00698939.
XX
PA (CETU) CETUS CORP.
XX
PI Mark DF, Lin LS, Lu SDY, Wang AM;
XX
DR WPI; 1986-225458/34.
DR P-PSDB; AAP60655.
XX
PT New synthetic muteins of human tumour necrosis factor protein - are obtd.
PT by direct mutagenesis and retain antitumour activity.
XX
PS Disclosure; Fig 1; 47pp; English.
XX
CC The sequence encoding TNF produced by the promyelocytic leukemia cell
CC line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see
CC AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
CC sequence appears to be involved in disulphide linkages. The patentors
CC claim a novel synthetic mutein of a biologically active hTNF protein,
CC having at least one cysteine residue free from a disulphide link and non-
CC essential to the activity and having at least one of the cysteine
CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
CC claimed
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 1; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1106

RESULT 13
ACA64836
ID ACA64836 standard; DNA; 1585 BP.
XX
AC ACA64836;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human TNF-alpha DNA corresponding to M10988.
XX
KW Human; chronic inflammatory joint disease; infection; tumour;
KW antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW immunosuppressive; gene therapy; etioloical pathogenicity; ds.
XX
OS Homo sapiens.
XX
PN DE10127572-A1.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2001; 2001DE-01027572.
XX

PR 30-MAY-2001; 2001DE-01027572.
XX (PATH-) PATHOARRAY GMBH.
PA
XX Haeupl T, Ungethuen U, Blaess S;
PI WPI; 2003-240797/24.
XX
DR Reagents for diagnosis, study and therapy of chronic inflammatory joint
XX and other diseases, comprises any of many specified genes or derived
PT proteins.
PT
XX Claim 1; Page; 12pp; German.
PS
XX This invention describes a novel reagent for diagnosis, molecular
CC definition and therapy of chronic inflammatory joint diseases, and other
CC inflammatory disorders, infective or tumour diseases in humans. The
CC products of the invention have antiinflammatory, cytostatic,
CC antiarthritic, antirheumatic and immunosuppressive activity and can be
CC used for gene therapy. The reagent of the invention and any proteins and
CC antibodies derived from it, are used (i) for analysing tissue and blood
CC samples for medical diagnosis; (ii) for diagnosis and characterisation of
CC chronic joint diseases, on the basis of molecular characterisation, and
CC determining the etiological pathogenicity principle of as yet
CC uncharacterised inflammatory diseases, also monitoring progression and/or
CC treatment of disease, and optimisation of therapy and (iii) for
CC developing treatments for inflammatory diseases, particularly of joints,
CC infections and tumours. ACA64801-ACA64965 represent human polynucleotides
CC used in the method of the invention
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 8; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
QY 61 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 1106
RESULT 14
ADF76346
ID ADF76346 standard; cDNA; 1585 BP.
XX
AC ADF76346;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein cDNA SeqID 19.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuro peptide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
XX
OS Homo sapiens.
XX
PN WO2003072035-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005241.
XX
PR 22-FEB-2002; 2002US-0359461P.
XX
PA (GETH) GENENTECH INC.
XX

PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
DR WPI; 2003-721702/68.
DR P-PSDB; ADF76347.
XX
PT New PRO polypeptides, useful for diagnosing and treating an immune
PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
PT diabetes mellitus.
XX
PS Claim 2; SEQ ID NO 19; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuro peptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 10; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
QY 61 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 104
Db 1063 GAATCTGGAGACCAGGAGCCCTTGGTTCTGGCCAGAAATGCTGC 1106
RESULT 15
ADI32003
ID ADI32003 standard; cDNA; 1585 BP.
XX
AC ADI32003;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CDNA #1329.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
PN US6607879-B1.
XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.

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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 23:36:03 ; Search time 2377.85 Seconds
(without alignments)
1664.816 Million cell updates/sec

Title: US-09-801-371A-1
Perfect score: 104
Sequence: 1 gaattcaaaactggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	474	5 BX118951	BX118951 BX118951
C 2	104	100.0	630	6 CB528492	CB528492 UI-H-FT2-
C 3	104	100.0	645	6 CD370363	CD370363 UI-H-FT1-
C 4	104	100.0	688	6 CD367676	CD367676 UI-H-FT1-
C 5	104	100.0	696	6 CA307225	CA307225 UI-H-FT1-
C 6	104	100.0	699	6 CD364761	CD364761 UI-H-FT2-
C 7	104	100.0	703	6 CD368142	CD368142 UI-H-FT1-
C 8	104	100.0	713	6 CA308256	CA308256 UI-H-FT1-
C 9	104	100.0	719	6 CB528694	CB528694 UI-H-FT2-
C 10	104	100.0	722	5 BQ007008	BQ007008 UI-H-E11-
C 11	104	100.0	722	6 CA307062	CA307062 UI-H-FT1-
C 12	104	100.0	722	6 CD364988	CD364988 UI-H-FT2-
C 13	104	100.0	723	6 CA308777	CA308777 UI-H-FT1-
C 14	104	100.0	723	6 CD368116	CD368116 UI-H-FT1-
C 15	104	100.0	724	6 CA309711	CA309711 UI-H-FT1-
C 16	104	100.0	726	6 CA310368	CA310368 UI-H-FT1-
C 17	104	100.0	726	6 CD368929	CD368929 UI-H-FT1-
C 18	104	100.0	742	6 CA309509	CA309509 UI-H-FT1-
C 19	104	100.0	744	6 CD366187	CD366187 UI-H-FT1-
C 20	104	100.0	748	6 CA306559	CA306559 UI-H-FT1-
C 21	104	100.0	1068	1 AL543083	AL543083 AL543083
C 22	103	99.0	248	7 T29839	T29839 EST97164 Hu
C 23	103	99.0	693	6 CD367625	CD367625 UI-H-FT1-
C 24	102.4	98.5	684	6 CA307429	CA307429 UI-H-FT1-

C 25	102.4	98.5	713	6 CA309664	CA309664 UI-H-FT1-
C 26	102.4	98.5	718	6 CD367794	CD367794 UI-H-FT1-
C 27	100.8	96.9	672	6 CD367664	CD367664 UI-H-FT1-
C 28	92	88.5	755	6 CD240146	CD240146 DTL3P2G5
C 29	86	82.7	581	1 AI242177	AI242177 qh81g08.x
C 30	85	81.7	561	4 BG232086	BG232086 naf32e06.
C 31	68.2	65.6	583	6 CA748748	CA748748 UI-H-FT1-
C 32	61.4	59.0	1011	1 AL575811	AL575811 AL575811
C 33	61.2	58.8	564	1 AA699697	AA699697 z178f12.8
C 34	60.8	58.5	562	1 AA207062	AA207062 zr87b03.8
C 35	48.2	46.3	546	1 AA824594	AA824594 oc83d11.8
C 36	34.8	33.5	136	8 B38591	B38591 HS-1047-B2-
C 37	32.6	31.3	691	1 AL110410	AL110410 DKF2p434K
C 38	32.6	31.3	888	5 BQ232100	BQ232100 AGENCOURT
C 39	32.2	31.0	342	2 BF407522	BF407522 UI-R-BJ2-
C 40	31.8	30.6	876	9 CNS001YJ	AL075400 Drosophil
C 41	30.6	29.4	652	9 CE210980	CE210980 tigr-g88-
C 42	30.6	29.4	701	7 CO049356	CO049356 Le mx0 11
C 43	30.6	29.4	792	7 CK777347	CK777347 964375-MA
C 44	30.4	29.2	430	6 CA563031	CA563031 K0308C04-
C 45	30.4	29.2	446	2 BB840094	BB840094 BB840094

ALIGNMENTS

RESULT 1
BX118951
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BX118951 474 bp mRNA linear EST 10-FEB-2003
BX118951 Soares fetal heart NBHH19W Homo sapiens cDNA clone
IMAGp998L124300 ; IMAGE:1693595, mRNA sequence.
BX118951
BX118951.1 GI:27882696
EST.
Homo sapiens (human)
Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3
Unpublished (2003)
Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998L124300.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.

FEATURES
source

Location/Qualifiers
1..474
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998L124300 ; IMAGE:1693595"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal heart_NBHH19W"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

ORIGIN

Query Match 100.0%; Score 104; DB 5; Length 474;
Best Local Similarity 100.0%; Pred. No. 2.7e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 65 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 124
|||||
QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 125 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 168
|||||

RESULT 2
CB528492/c

LOCUS CB528492 630 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT2-bjd-e-20-0-UI.s1 NCI CGAP FT2 Homo sapiens cDNA clone
UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.

ACCESSION CB528492
VERSION CB528492.1 GI:29388228
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 630)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 1-29, >ATrich#Low_complexity (matched complement) 205-279, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source 1..630
Location/Qualifiers
1..630
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjd-e-20-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_FT2 is a subtraced cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library

construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtraced according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCGC"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 503 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 444
|||||
QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 443 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 400
|||||

RESULT 3

CD370363/c

LOCUS

DEFINITION CD370363 645 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bkb-n-03-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bkb-n-03-0-UI 3', mRNA sequence.

ACCESSION CD370363
VERSION CD370363.1 GI:31154453
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 645)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES source 1..645
Location/Qualifiers
1..645
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bkb-n-03-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;

NCI_CGAP_FTI1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 645;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 592 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 533
|||||

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
|||||

Db 532 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 489
|||||

RESULT 4

CD367676/c
LOCUS CD367676 688 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bjr-1-14-0-UI.s1 NCI_CGAP_FTI1 Homo sapiens cDNA clone
UI-H-FT1-bjr-1-14-0-UI 3', mRNA sequence.

ACCESSION CD367676
VERSION CD367676.1 GI:31151766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 688)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA

sequence: 69-143, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source Location/Qualifiers
1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjr-1-14-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FTI1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI_CGAP_FTI1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 688;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||

Db 367 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 308
|||||

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
|||||

Db 307 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 264
|||||

RESULT 5

CA307225/c
LOCUS CA307225 696 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bhu-n-04-0-UI.s1 NCI_CGAP_FTI1 Homo sapiens cDNA clone
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.

ACCESSION CA307225
VERSION CA307225.1 GI:24470279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 696)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1. .696
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-n-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.8e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 594 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 535
|||||
QY 61 GAATCTGGAGACCAGGAGCCTTGGTTCTGGCCAGAAATGCTGC 104

Db 534 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 491
|||||
RESULT 6
CD364761/c
LOCUS
DEFINITION UI-H-FT2-bjm-j-11-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.
ACCESSION CD364761
VERSION CD364761.1 GI:31148851
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 699)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
source
1. .699
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjm-j-11-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP_FT2 is a subtraced cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtraced according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
ORIGIN
Query Match 100.0%; Score 104; DB 6; Length 699;

Best Local Similarity 100.0%; Pred. No. 2.9e-21; Mismatches 0; Indels 0; Gaps 0; Matches 104; Conservative 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 594 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 535
|||||

Qy 61 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 534 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 491
|||||

RESULT 7
CD368142/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD368142 703 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bjv-e-20-0-UI.s1 NCI CGAP_Ft1 Homo sapiens cDNA clone
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.
CD368142
CD368142.1 GI:31152232
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 298-372, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-e-20-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ft1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was

primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 596 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 537
|||||

Qy 61 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 536 GAATCTGGAGACGAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 493
|||||

RESULT 8
CA308256/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CA308256 713 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bhy-e-14-0-UI.s1 NCI CGAP_Ft1 Homo sapiens cDNA clone
UI-H-FT1-bhy-e-14-0-UI 3', mRNA sequence.
CA308256
CA308256.1 GI:24471310
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..713
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-e-14-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ft1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)

Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5846517"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_E11"

/note="Organ: Left Pélvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_E11 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACCTTGCAC.

TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-E11
TAG_SEQ=ACACCTTGCAC"

ORIGIN

Query Match 100.0%; Score 104; DB 5; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 595 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

Qy 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 535 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 492

RESULT 11
CA307062/c

LOCUS CA307062 722 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bhu-o-04-0-UI.s1 NCI CGAP_Ft1 Homo sapiens cDNA clone
UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.

ACCESSION CA307062
VERSION CA307062.1 GI:24470116
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)

REFERENCE 1 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA
sequence: 295-369, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-o-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_Ft1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP_Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 593 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 534

Qy 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 533 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 490

RESULT 12
CD364988/c

LOCUS CD364988 722 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT2-bjn-c-04-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.
ACCESSION CD364988
VERSION CD364988.1 GI:31149078
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1. .722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-c-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 104; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 595 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
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Db 535 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 492

RESULT 13
CA308777/c

LOCUS
DEFINITION UI-H-FT1-bhy-b-23-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.
ACCESSION CA308777
VERSION CA308777.1 GI:24471831
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 723)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1. .723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

	Query Match	100.0%;	Score 104;	DB 6;	Length 723;
	Best Local Similarity	100.0%;	Pred. No. 2.9e-21;		
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		'			
Db	595	GAATTCAAAC	TGGGGCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG		
Qy	61	GAATCTGGAGACC	AGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	104	
Db	535	GAATCTGGAGACC	AGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	492	

RESULT 14	CD368116/c	CD368116	723 bp	linear	EST 05-AUG-2004
LOCUS	UI-H-FT1-bjv-a-04-0-UI.s1	NCI CGAP_FTI	Homo sapiens	clone	
DEFINITION	UI-H-FT1-bjv-a-04-0-UI 3', mRNA sequence.				
ACCESSION	CD368116				
VERSION	CD368116.1	GI:31152206			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 723)				
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgaps-r@mail.nih.gov				
	Tissue Procurement: Dr. Gary W. Hunninghake, U of I				
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa				
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa				
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa				
	Clone Distribution: Distribution information can be found at				
	http://genome.uiowa.edu/distribution/cgap.html				
	The following repetitive elements were found in this cDNA				
	sequence: 297-371, >(TAAA)n#Simple_repeat				
	Seq primer: M13 FORWARD				
	POLYA=Yes.				

FEATURES

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Location/Qualifiers
1. .723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-a-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ft1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site:1: EcoR I; Site 2: Not I;
NCI_CGAP_Ft1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome

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Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCGC. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCGC"

ORIGIN									
Query Match	100.0%	Score 104;	DB 6;	Length 723;					
Best Local Similarity	100.0%	Pred. No. 2.9e-21;							
Matches 104; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;		
QY	1	GAATTCAAAC	TGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG	60					
Db	595	GAATTCAAAC	TGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG	536					
QY	61	GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC	104						
Db	535	GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC	492						
RESULT 15									
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LOCUS									
DEFINITION									
UI-H-FTL1-b1c-b-17-0-UI.s1 NCI CGAP_FTL1 Homo sapiens cDNA clone									
UI-H-FTL1-b1c-b-17-0-UI 3', mRNA sequence.									
CA309711									
724 bp mRNA linear EST 05-AUG-2004									

CA309711 724 bp mRNA linear EST 05-AUG-2004
 UI-H-FT1-b1c-b-17-0-UI.s1 NCI_CGAP_FTI Homo sapiens cDNA clone
 UI-H-FT1-b1c-b-17-0-UI 3', mRNA sequence.
 CA309711
 CA309711.1 GI:24472765
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 724)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Dr. Gary W. Hunninghake, U of I
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 297-371, >(TAAA)n#Simple_repeat
 Seq primer: M13 FORWARD
 POLYA=Yes.

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FEATURES
source
Location/Qualifiers
1. .724
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-Ftl1-bic-b-17-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ftl1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI_CGAP_Ftl1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to

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incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match		100.0%	Score 104;	DB 6;	Length 724;
Best Local Similarity		100.0%	Pred. No. 2.9e-21;		
Matches	104;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY	1	GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60			
Db	595	GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536			
QY	61	GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104			
Db	535	GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 492			

Search completed: September 3, 2005, 02:11:40
Job time : 2384.85 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 13:14:57 ; Search time 424.49 Seconds
(without alignments)
400.888 Million cell updates/sec

Title: US-09-801-371A-1
Perfect score: 104
Sequence: 1 gaattcaaaactggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	104	100.0	787	4 US-09-032-297A-13	Sequence 13, Appl
2	104	100.0	787	4 US-09-229-151C-7	Sequence 7, Appli
3	104	100.0	1585	4 US-09-023-655-1329	Sequence 1329, Ap
4	104	100.0	1587	4 US-09-949-016-5156	Sequence 5156, Ap
5	104	100.0	1643	3 US-08-880-342-36	Sequence 36, Appl
6	104	100.0	1643	3 US-09-505-250-4	Sequence 4, Appli
7	104	100.0	2270	4 US-09-229-151C-13	Sequence 13, Appl
8	104	100.0	2570	4 US-09-229-151C-14	Sequence 14, Appl
9	104	100.0	3634	3 US-09-166-186-1	Sequence 1, Appli
10	104	100.0	3634	3 US-09-313-932-1	Sequence 1, Appli
11	104	100.0	3634	3 US-09-109-663-34	Sequence 34, Appl
12	104	100.0	6682	4 US-09-949-016-16898	Sequence 16898, A
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14	32.6	31.3	2623	4 US-09-976-594-142	Sequence 142, App
15	29.2	28.1	601	4 US-09-949-016-182065	Sequence 182065,
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17	29	27.9	7517	4 US-09-949-016-15603	Sequence 15603, A
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19	28	26.9	28720	3 US-09-341-587-7	Sequence 7, Appli
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26	27.4	26.3	124264	4 US-09-949-016-16396	Sequence 16396, A
27	27.2	26.2	412	4 US-09-621-976-19072	Sequence 19072, A

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	37	26.6	25.6	767677	4	US-09-949-016-12147	Sequence 12147, A
	38	26.6	25.6	767677	4	US-09-949-016-17361	Sequence 17361, A
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	42	26.4	25.4	3171	4	US-09-169-768-15	Sequence 15, Appl
	43	26.4	25.4	3181	1	US-08-655-086-1	Sequence 1, Appli
	44	26.4	25.4	3349	4	US-09-169-768-13	Sequence 13, Appl
	45	26.4	25.4	3531	4	US-09-169-768-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION:
; APPLICANT: Revati J. Tatake, Steven D. Marlin and
; Randall W. Barton
; TITLE OF INVENTION: Self-Regulated Apoptosis of
; Inflammatory Cells by Gene Therapy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Boehringer Ingelheim Corporation
; STREET: 900 Ridgebury Road, P.O. Box 368
; CITY: Ridgefield
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06877-0368
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,297A
; FILING DATE: 27-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,266
; FILING DATE: 28-FEB-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert P. Raymond
; REGISTRATION NUMBER: 25089
; REFERENCE/DOCKET NUMBER: 9/121PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-791-6183
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: DNA
; FEATURE:
; NAME/KEY: TNFa 3', untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-032-297A-13

Query Match 100.0%; Score 104; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.2e-27;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

Query Match 100.0%; Score 104; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 222 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
|||||
Db 282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 325

RESULT 3
US-09-023-655-1329
; Sequence 1329, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g339737
US-09-023-655-1329

Query Match 100.0%; Score 104; DB 4; Length 1585;
Best Local Similarity 100.0%; Pred. No. 5.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 1003 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
|||||
Db 1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 1106

RESULT 4
US-09-949-016-5156
; Sequence 5156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5156
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5156

Query Match 100.0%; Score 104; DB 4; Length 1587;
Best Local Similarity 100.0%; Pred. No. 5.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 1005 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1064

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 104
|||||
Db 1065 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCAGAAATGCTGC 1108

RESULT 5
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1643 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: TNF cDNA HSTNFR (EMBL Accession
; INDIVIDUAL ISOLATE: #X01394)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..851
US-08-880-342-36

Query Match 100.0%; Score 104; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 5.5e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCAGGGAGCCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||
Db 1130 GAATCTGGAGACCAGGGAGCCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 6
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (153)...(854)
US-09-505-250-4

Query Match 100.0%; Score 104; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 5.5e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||
Db 1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCAGGGAGCCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||
Db 1130 GAATCTGGAGACCAGGGAGCCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 7
US-09-229-151C-13
; Sequence 13, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 13
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR
US-09-229-151C-13

Query Match 100.0%; Score 104; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 6.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||
Db 1705 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1764

QY 61 GAATCTGGAGACCAGGGAGCCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||
Db 1765 GAATCTGGAGACCAGGGAGCCCTTTGGTTCTGGCCAGAAATGCTGC 1808

```
RESULT 8
US-09-229-151C-14
; Sequence 14, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tataka, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 14
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -1005TNFPGB3'UTR
US-09-229-151C-14

Query Match      100.0%; Score 104; DB 4; Length 2570;
Best Local Similarity 100.0%; Pred. No. 6.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||||||
Db      2005 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2064
      |||||||

QY      61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
      |||||||
Db      2065 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2108
      |||||||

RESULT 9
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
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; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
; TITLE: homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

Query Match      100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.3e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
      |||||||
Db      2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867
      |||||||

QY      61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
      |||||||
Db      2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2911
      |||||||

RESULT 10
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
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LOCATION: (1635)..(1821)
FEATURE:
NAME/KEY: exon
LOCATION: (1822)..(1869)
FEATURE:
NAME/KEY: intron
LOCATION: (1870)..(2070)
FEATURE:
NAME/KEY: exon
LOCATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Pennica, D.
AUTHORS: Goeddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes:
TITLE: structure, homology and chromosomal localization
JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
PAGES: 6361-6373
DATE: 1985-09-11
DATABASE ACCESSION NUMBER: X02910 Genbank
DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match 100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.3e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 11
US-09-109-663-34
Sequence 34, Application US/09109663
Patent No. 6277981
GENERAL INFORMATION:
APPLICANT: Tu, Guang-Chou
APPLICANT: Israel, Yedy
TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
FILE REFERENCE: 9855-3U1
CURRENT APPLICATION NUMBER: US/09/109,663
CURRENT FILING DATE: 1998-07-03
EARLIER APPLICATION NUMBER: 60/051,705
EARLIER FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 3634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

Query Match 100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.3e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||

Db 2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867

Qy 61 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 2868 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2911

RESULT 12
US-09-949-016-16898
Sequence 16898, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16898
LENGTH: 6682
TYPE: DNA
ORGANISM: Human
US-09-949-016-16898

Query Match 100.0%; Score 104; DB 4; Length 6682;
Best Local Similarity 100.0%; Pred. No. 9e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
|||||
Db 4099 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 4158

Qy 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
|||||
Db 4159 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 4202

RESULT 13
US-09-376-774-5/c
Sequence 5, Application US/09376774
Patent No. 6759236
GENERAL INFORMATION:
APPLICANT: Fung, Yuen Kai
APPLICANT: Gomer, Charles
APPLICANT: T'Ang, Anne
TITLE OF INVENTION: Methods To Enhance And Confine Expression
TITLE OF INVENTION: Of Genes
FILE REFERENCE: D6087
CURRENT APPLICATION NUMBER: US/09/376,774
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/096,947
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5
LENGTH: 10728
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: recombinant vector pPATH-TNF?
US-09-376-774-5

Query Match 100.0%; Score 104; DB 4; Length 10728;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db 4220 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 4161

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db 4160 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 4117

RESULT 14
US-09-976-594-142/c
; Sequence 142, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 142
; LENGTH: 2623
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 337187.1
; NAME/KEY: unsure
; LOCATION: 2612
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-142

Query Match 31.3%; Score 32.6; DB 4; Length 2623;
Best Local Similarity 58.9%; Pred. No. 0.14;
Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 9 ACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATCTGG 68
Db 359 ACTGGGTGCTGAGGTAGTAGCGGGGCTGTGCCTGCCTGCCCTCCCGCTTGGAGGGG 300

QY 69 AGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTG 103
Db 299 AGCCCTGAGGGCCTCTGGGGCTGGCCTGGAAGTG 265

RESULT 15
US-09-949-016-182065
; Sequence 182065, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182065
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-182065

Query Match 28.1%; Score 29.2; DB 4; Length 601;
Best Local Similarity 65.2%; Pred. No. 1.4;
Matches 43; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 6 CAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATC 65
Db 355 CAGACTGTGCCACGACAGACTCCCTGGGGGCTTTTCTTTTCCACCTCAGATATTTTGAAC 414

QY 66 TGGAGA 71
Db 415 TGAAGA 420

Search completed: September 2, 2005, 18:55:18
Job time : 428.49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 15:27:57 ; Search time 478.966 Seconds
(without alignments)
1421.994 Million cell updates/sec

Title: US-09-801-371A-1
Perfect score: 104
Sequence: 1 gaattcaactggggcctcc.....ggttctggccagaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	104	100.0	104	9 US-09-801-371A-5	Sequence 5, Appli
3	104	100.0	787	18 US-10-356-308A-13	Sequence 13, Appl
4	104	100.0	798	21 US-10-895-393-9	Sequence 9, Appli
5	104	100.0	806	20 US-10-814-634A-5	Sequence 5, Appli
6	104	100.0	1585	17 US-10-172-118-501	Sequence 501, App
7	104	100.0	1585	18 US-10-342-887-501	Sequence 501, App

8	104	100.0	1585	18	US-10-641-643-1329	Sequence 1329, Ap
9	104	100.0	1585	20	US-10-370-715B-19	Sequence 19, Appl
10	104	100.0	1643	15	US-10-272-411-4	Sequence 4, Appli
11	104	100.0	1643	15	US-10-218-547-3	Sequence 3, Appli
12	104	100.0	1643	15	US-10-272-328A-4	Sequence 4, Appli
13	104	100.0	1643	16	US-10-310-793-9	Sequence 9, Appli
14	104	100.0	1643	17	US-10-172-118-1901	Sequence 1901, Ap
15	104	100.0	1643	18	US-10-342-887-1901	Sequence 1901, Ap
16	104	100.0	1643	20	US-10-475-024-6	Sequence 6, Appli
17	104	100.0	1643	21	US-10-929-182-1	Sequence 1, Appli
18	104	100.0	1643	22	US-10-475-026-6	Sequence 6, Appli
19	104	100.0	1666	16	US-10-247-671-68	Sequence 68, Appl
20	104	100.0	1666	20	US-10-799-345-17	Sequence 17, Appl
21	104	100.0	1669	20	US-10-688-845-74	Sequence 74, Appl
22	104	100.0	2088	9	US-09-973-850-1	Sequence 1, Appli
23	104	100.0	2088	9	US-09-973-850-2	Sequence 2, Appli
24	104	100.0	2088	9	US-09-973-850-3	Sequence 3, Appli
25	104	100.0	3634	10	US-09-824-322B-1	Sequence 1, Appli
26	104	100.0	3634	10	US-09-932-300-34	Sequence 34, Appl
27	104	100.0	3634	17	US-10-191-997-104	Sequence 104, App
28	104	100.0	3634	18	US-10-202-062-3	Sequence 3, Appli
29	104	100.0	3634	19	US-10-652-795-1	Sequence 1, Appli
30	104	100.0	3634	21	US-10-647-918-1	Sequence 1, Appli
31	104	100.0	3634	21	US-10-770-970-1	Sequence 1, Appli
32	104	100.0	3634	24	US-11-028-780-3	Sequence 3, Appli
33	104	100.0	4830	17	US-10-429-802-33	Sequence 33, Appl
34	104	100.0	4830	17	US-10-430-503-24	Sequence 24, Appl
35	104	100.0	14036	21	US-10-741-600-17806	Sequence 17806, A
36	104	100.0	14769	21	US-10-741-600-18012	Sequence 18012, A
c 37	104	100.0	22173	19	US-10-322-696-28	Sequence 28, Appl
38	93	89.4	1279	16	US-10-247-671-120	Sequence 120, App
39	77	74.0	81	9	US-09-801-371A-7	Sequence 7, Appli
40	59.8	57.5	3673778	16	US-10-312-841-1	Sequence 1, Appli
c 41	58.2	56.0	3673778	16	US-10-312-841-2	Sequence 2, Appli
42	50	48.1	50	9	US-09-801-371A-8	Sequence 8, Appli
43	43	41.3	43	9	US-09-801-371A-2	Sequence 2, Appli
c 44	43	41.3	43	9	US-09-801-371A-6	Sequence 6, Appli
45	42	40.4	418	9	US-09-796-692-6223	Sequence 6223, Ap

ALIGNMENTS

RESULT 1
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match 100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      61  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
      |||||||
Db      61  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
      |||||||

RESULT 2
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5

Query Match      100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAATCAAAGTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db      104  GAAATCAAAGTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 45

QY      61  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
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Db      44  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1
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RESULT 3
US-10-356-308A-13
; Sequence 13, Application US/10356308A
; Publication No. US20040039186A1
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall Wilber
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/121-1-CIP1
; CURRENT APPLICATION NUMBER: US/10/356,308A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/032,297
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,266
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 1 to 787
; OTHER INFORMATION: TNFa 3' untranslated region
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E., et al.
; JOURNAL: Nucleic Acid Research
; VOLUME: 13
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; PAGES: 6361-6373
; DATE: 1985
US-10-356-308A-13

Query Match      100.0%; Score 104; DB 18; Length 787;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAATCAAAGTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db      222  GAAATCAAAGTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281

QY      61  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
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Db      282  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 325

RESULT 4
US-10-895-393-9
; Sequence 9, Application US/10895393
; Publication No. US20050048549A1
; GENERAL INFORMATION:
; APPLICANT: CAO, Liangxian
; APPLICANT: MEHTA, Anuradha
; APPLICANT: NARYSHKIN, Nikolai A.
; APPLICANT: PELLEGRINI, Matthew C.
; APPLICANT: ROMFO, Charles M.
; APPLICANT: TRIFILLIS, Panayiota
; APPLICANT: TROTTA, Christopher R.
; TITLE OF INVENTION: Methods and Agents for Screening for Compounds Capable of Modulat
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 19025.012
; CURRENT APPLICATION NUMBER: US/10/895,393
; CURRENT FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: PCT/US04/01643
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/441,637
; PRIOR FILING DATE: 2003-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-895-393-9

Query Match      100.0%; Score 104; DB 21; Length 798;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAATCAAAGTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db      216  GAAATCAAAGTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 275

QY      61  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
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Db      276  GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 319

RESULT 5
US-10-814-634A-5
; Sequence 5, Application US/10814634A
; Publication No. US20040231007A1
; GENERAL INFORMATION:
; APPLICANT: CHENEVAL, Dominique
; APPLICANT: KASTELIC, Tania
; APPLICANT: Novation Pharmaceuticals Inc.
; TITLE OF INVENTION: Assay for Identifying Compounds Which
; TITLE OF INVENTION: Affect Stability of mRNA
; FILE REFERENCE: 793-104CIP
; CURRENT APPLICATION NUMBER: US/10/814,634A
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; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: US 09/869,159
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: GB 9828709.7
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-814-634A-5

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Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 227 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 286
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QY 61 GAATCTGGAGACCAGGAGGCCTTTGGTTCTGGCCAGAAATGCTGC 104
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Db 287 GAATCTGGAGACCAGGAGGCCTTTGGTTCTGGCCAGAAATGCTGC 330
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RESULT 6
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_000594
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501

Query Match      100.0%; Score 104; DB 17; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAATCTGGAGACCAGGAGGCCTTTGGTTCTGGCCAGAAATGCTGC 104
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Db 1063 GAATCTGGAGACCAGGAGGCCTTTGGTTCTGGCCAGAAATGCTGC 1106
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RESULT 7
US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
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; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-501

Query Match      100.0%; Score 104; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db 1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
   |||||||

QY 61 GAATCTGGAGACCAGGAGGCCTTTGGTTCTGGCCAGAAATGCTGC 104
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Db 1063 GAATCTGGAGACCAGGAGGCCTTTGGTTCTGGCCAGAAATGCTGC 1106
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RESULT 8
US-10-641-643-1329
; Sequence 1329, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1585 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g339737
; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329

Query Match          100.0%; Score 104; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db 1003 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCCGAATGCTGC 104
   |||||||
Db 1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCCGAATGCTGC 1106

RESULT 9
US-10-370-715B-19
; Sequence 19, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;   Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNET
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 19
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-19

Query Match          100.0%; Score 104; DB 20; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db 1003 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCCGAATGCTGC 104
   |||||||
Db 1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCCGAATGCTGC 1106

RESULT 10
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
```

```
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match          100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
   |||||||
Db 1070 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCCGAATGCTGC 104
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Db 1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTTGCCCGAATGCTGC 1173

RESULT 11
US-10-218-547-3
; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-218-547-3

Query Match          100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Db	1070	GAATTCAAAC	TGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG	1129
QY	61	GAATCTGGAGAC	CAGGGAGCCTTTTGGTTCTGGCCAGAAATGCTGC	104
Db	1130	GAATCTGGAGAC	CAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC	1173

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RESULT 12
US-10-272-328A-4
; Sequence 4, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-272-328A-4

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	Query Match	100.0%;	Score 104;	DB 15;	Length 1643;
	Best Local Similarity	100.0%;	Pred. No. 8.1e-28;		
	Matches 104;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GAATTCAAAC	TGGGCGCTCCAGAACTCACTGGGGCTACAGCTTTTGATCCCTGACATCTG	60	
Db	1070	GAATTCAAAC	TGGGCGCTCCAGAACTCACTGGGGCTACAGCTTTTGATCCCTGACATCTG		
Qy	61	GAATCTGGAG	ACCAGGGAGCCTTTTGGTTCTGGCCAGAATGCTGC	104	
Db	1130	GAATCTGGAG	ACCAGGGAGCCTTTTGGTTCTGGCCAGAATGCTGC	1173	

RESULT 13
US-10-310-793-9
; Sequence 9, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27

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; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1i
; SEQ ID NO 9
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
; US-10-310-793-9

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	Best Local Similarity	100.0%	Pred. No. 8.1e-28;		
	Matches 104;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG	60		
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Qy	61	GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC	104		
Db	1130	GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC	1173		

RESULT 14
US-10-172-118-1901
; Sequence 1901, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14 ;
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: X01394
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1901

	Query Match	100.0%	Score 104;	DB 17;	Length 1643;
	Best Local Similarity	100.0%	Pred. No. 8.1e-28;		
	Matches 104; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTTGATCCCTGACATCTG	60		
Db	1070	GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTTGATCCCTGACATCTG	1129		
Qy	61	GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC	104		
Db	1130	GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC	1173		

RESULT 15
US-10-342-887-1901
; Sequence 1901, Application US/10342887

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; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1901

Query Match      100.0%; Score 104; DB 18; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.1e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Db      1070 GAATTCAAACCTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129

QY      61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
Db      1130 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

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OM nucleic - nucleic search, using sw model

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Perfect score: 43
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	43	100.0	400	11	GI3533	GI3533 SHGC-11076
2	43	100.0	787	6	BD137681	BD137681 Self-regu
3	43	100.0	787	6	AR300453	AR300453 Sequence
4	43	100.0	787	6	BD070551	BD070551 Self-regu
5	43	100.0	817	6	A16444	A16444 Xho-PstI fr
6	43	100.0	817	6	E02109	E02109 DNA sequenc
7	43	100.0	1047	9	HSA249755	AJ249755 Homo sapi
8	43	100.0	1275	6	I08430	I08430 Sequence 5
9	43	100.0	1323	6	I07953	I07953 Sequence 6
10	43	100.0	1324	6	E00702	E00702 cDNA encodi
11	43	100.0	1324	6	I03610	I03610 Sequence 2
12	43	100.0	1379	12	SYNTNFTRP	M35592 Synthetic h
13	43	100.0	1465	6	I04244	I04244 Sequence 2
14	43	100.0	1560	6	I08863	I08863 Sequence 3
15	43	100.0	1585	6	A37272	A37272 Sequence 12
16	43	100.0	1585	6	I04169	I04169 Sequence 1
17	43	100.0	1585	6	I04198	I04198 Sequence 1
18	43	100.0	1585	6	I08384	I08384 Sequence 5
19	43	100.0	1585	6	I08429	I08429 Sequence 3

20	43	100.0	1585	6	AR380784	AR380784 Sequence
21	43	100.0	1585	9	HUMTNFAA	M10988 Human tumor
22	43	100.0	1606	6	I07541	I07541 Sequence 22
23	43	100.0	1643	6	AR146199	AR146199 Sequence
24	43	100.0	1643	6	AR366225	AR366225 Sequence
25	43	100.0	1643	9	HSTNFR	X01394 Human mRNA
26	43	100.0	1676	9	BC028148	BC028148 Homo sapi
27	43	100.0	2270	6	BD137687	BD137687 Self-regu
28	43	100.0	2270	6	AR300459	AR300459 Sequence
29	43	100.0	2570	6	BD137688	BD137688 Self-regu
30	43	100.0	2570	6	AR300460	AR300460 Sequence
31	43	100.0	3103	9	HUMTNFX	M26331 Human tumor
32	43	100.0	3634	6	AR100270	AR100270 Sequence
33	43	100.0	3634	6	AR149925	AR149925 Sequence
34	43	100.0	3634	6	BD227798	BD227798 Antisense
35	43	100.0	3634	6	BD271232	BD271232 Predictio
36	43	100.0	3634	6	BD064008	BD064008 Novel exp
37	43	100.0	3634	9	HSTNFA	X02910 Human gene
38	43	100.0	4830	9	AY066019	AY066019 Homo sapi
39	43	100.0	6974	9	AB088112	AB088112 Homo sapi
40	43	100.0	7112	6	AX100950	AX100950 Sequence
41	43	100.0	7112	6	AX100965	AX100965 Sequence
42	43	100.0	7112	9	HUMTNFAB	M16441 Human tumor
43	43	100.0	7240	9	AY214167	AY214167 Homo sapi
C 44	43	100.0	10728	6	AR562497	AR562497 Sequence
C 45	43	100.0	16310	9	HSTNFABX	Z15026 Homo sapien

ALIGNMENTS

RESULT 1

GI3533
LOCUS SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
DEFINITION SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
ACCESSION GI3533
VERSION GI3533.1 GI:1129272
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Olivier,M. and Cox,D.R.
TITLE Unpublished, Olivier, M., Cox, D.R. (2000)
JOURNAL Unpublished (2000)
COMMENT

Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5800
Fax: (650) 320-5801

Email: olivier@shgc.stanford.edu
Primer A: CACTAAGAATTCAAACCTGGGC
Primer B: GAGGAAGCCTAAGTCCAC
STS size: 166
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs derived from M10988 -- Unigene.

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/mol_type="genomic DNA"
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/map="6"
/clone_lib="Human"
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210. .231
complement(356.. .375)

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primer_bind

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Best Local Similarity 100.0%; Pred. No. 7.7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 220 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 262

RESULT 2
BD137681
LOCUS BD137681 787 bp DNA linear PAT 18-SEP-2002
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION BD137681
VERSION BD137681.1 GI:23232626
KEYWORDS JP 2002504381-A/7.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 787)
AUTHORS Tataka,R.J., Marlin,S.D. and Barton,R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: JP 2002504381-A 7 12-FEB-2002;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002504381-A/7
PD 12-FEB-2002
PF 12-JAN-1999 JP 2000533579
PR 27-FEB-1998 US 60/076316
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
C12N15/09,A61K31/7088,A61K48/00,A61P1/04,A61P3/10,A61P17/06, PC
A61P25/00,
PC A61P29/00,A61P43/00,C12N9/64,C12Q1/68//C12N5/10,C12N15/00, PC
C12N5/00
CC TNF-alpha untranslated region
FH KEY Location/Qualifiers
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1. .787
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Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 3
AR300453
LOCUS AR300453 787 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 7 from patent US 6537784.
ACCESSION AR300453
VERSION AR300453.1 GI:31687895
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 787)
AUTHORS Tataka,R.J., Marlin,S.D. and Barton,R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: US 6537784-A 7 25-MAR-2003;
FEATURES Location/Qualifiers
source 1. .787
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 4
BD070551
LOCUS BD070551 787 bp DNA linear PAT 27-AUG-2002
DEFINITION Self-regulated apoptosis of inflammatory cells by gene therapy.
ACCESSION BD070551
VERSION BD070551.1 GI:22616154
KEYWORDS JP 2001516210-A/13.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 787)
AUTHORS Tataka,R.J., Marlin,S.D. and Barton,R.W.
TITLE Self-regulated apoptosis of inflammatory cells by gene therapy
JOURNAL Patent: JP 2001516210-A 13 25-SEP-2001;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2001516210-A/13
PD 25-SEP-2001
PF 27-FEB-1998 JP 1998537909
PR 28-FEB-1997 US 60/039266
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC
A61K31/70,C07H21/04,C12N15/12,C12P19/34
CC Strandedness: Single;
CC Topology: Linear;
CC TNF alpha nontranslated region
FH KEY Location/Qualifiers
FT source 1. .787
FT /organism='Unidentified'.
FEATURES
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1. .787
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/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 787;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 5
A16444
LOCUS
DEFINITION Xho-PstI fragment from THP-I cells. linear PAT 05-OCT-1994
ACCESSION A16444
VERSION A16444.1 GI:641014
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Soma,G.I., Mizuno,D., Tsuji,Y. and Kobayashi,N.
TITLE Anti-aids preparation
JOURNAL Patent: EP 0450240-A 9 09-OCT-1991;
Soma, Gen-Ichiro; Mizuno, Den'ichi
FEATURES
source 1. .817
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 817;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758
|||||
RESULT 6
E02109
LOCUS
DEFINITION DNA sequence coding for anti-tumor polypeptide. linear PAT 29-SEP-1997
ACCESSION E02109
VERSION E02109.1 GI:2170351
KEYWORDS JP 1989256390-A/1.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 817)
AUTHORS Soma,G., Mizuno,D. and Tsuji,Y.
TITLE NOVEL DNA AND PRODUCTION THEREOF, NOVEL PLASMID HAVING SAME, NOVEL POLYPEPTIDE AND PRODUCTION THEREOF AND NOVEL ANTINEOPLASTIC AGENT FROM SAID POLYPEPTIDE
JOURNAL Patent: JP 1989256390-A 1 12-OCT-1989;
SOMA GENICHIRO, MIZUNO DENICHI
COMMENT PN JP 1989256390-A/1
PD 12-OCT-1989
PF 03-APR-1988 JP 1988081683
PI SOMA GENICHIRO, MIZUNO DENICHI, TSUJI YOSHIKI PC
C12N15/00,A61K37/24,C07K13/00,C12P21/02,C12R1:19); CC
strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: library=THP-1 cell;
FH Key Location/Qualifiers
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FT /product='Anti-tumor polypeptide'.
FT Location/Qualifiers
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source 1. .817
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ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 817;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758
|||||
RESULT 7
HSA249755
LOCUS
DEFINITION Homo sapiens TNF-alpha gene for tumor necrosis factor-alpha, 3', linear PRI 29-SEP-1999
UTR, country United Arab Emirates.
ACCESSION AJ249755
VERSION AJ249755.1 GI:6002308
KEYWORDS TNF-alpha gene; tumor necrosis factor-alpha.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Farhan,A.J., Pravica,V. and Hutchinson,I.V.
TITLE Identification of new rare variant of human TNF-alpha 3' UTR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1047)
AUTHORS Farhan,A.J.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research
Division, Manchester University, Medical School, Stopford Building,
Oxford Road, Manchester, M13 9PT, UNITED KINGDOM
FEATURES
source 1. .1047
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/country="United Arab Emirates"
/note="new rare variant"
gene 1. .1047
/gene="TNF-alpha"
3'UTR 1. .>1047
/gene="TNF-alpha"
variation 322
/gene="TNF-alpha"
/replace="t"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 225 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 267
|||||
RESULT 8
I08430
LOCUS
DEFINITION Sequence 5 from Patent WO 8604606. linear PAT 02-DEC-1994
ACCESSION I08430
VERSION I08430.1 GI:588860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1275)
AUTHORS Mark,D.F., Lin,L.S., Lu,S.-D.Y. and Wang,A.M.
TITLE CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR NECROSIS FACTOR PROTEINS
JOURNAL Patent: WO 8604606-A 5 14-AUG-1986;
FEATURES
source 1. .1275
Location/Qualifiers

JOURNAL Nucleic Acids Symp. Ser. 17, 131-134 (1986)
MEDLINE 87174864
PUBMED 3031624
COMMENT Original source text: Altered human leukemic B-cell line Ball-1, cDNA to mRNA, clone pM324-346.
FEATURES
source Location/Qualifiers
1. .1379
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
178. .879
/note="synthetic tumor necrosis factor precursor"
/codon_start=1
/transl_table=11
/protein_id="AAC42098.1"
/db_xref="GI:209486"
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QWLNRRANALLANGVELRDNLVVPSEGLYLIYSQVLFKQGQCPSTHVLTHTISRIA
VSYQTKVNLLSAIKSPCQRETPEGAEKWPYEPYILGGVFQLEKGDRLSAEINRPDYL
DFAESGQVYFGIIL"
sig_peptide 178. .399
/note="synthetic tumor necrosis factor signal peptide"
mat_peptide 400. .876
/product="synthetic tumor necrosis factor"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1100 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1142
RESULT 13
I04244
LOCUS I04244 1465 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 2 from Patent US 4677197.
ACCESSION I04244
VERSION I04244.1 GI:268725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1465)
AUTHORS Lin,L.S. and Yamamoto,R.
TITLE Purification method for tumor necrosis factor
JOURNAL Patent: US 4677197-A 2 30-JUN-1987;
Cetus Corporation; Emeryville, CA
FEATURES
source Location/Qualifiers
1. .1465
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 1465;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 887 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 929
RESULT 14
I08863
LOCUS I08863 1560 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 3 from Patent WO 8806625.
ACCESSION I08863
VERSION I08863.1 GI:588416
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Mark,D.F., Lin,L.S., Thomsom,J.W. and Yamamoto,R.
TITLE ARGININE-DEPLETED HUMAN TUMOR NECROSIS FACTOR
JOURNAL Patent: WO 8806625-A 3 07-SEP-1988;
FEATURES
source Location/Qualifiers
1. .1560
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 43; DB 6; Length 1560;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049
RESULT 15
A37272
LOCUS A37272 1585 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 12 from Patent WO9404196.
ACCESSION A37272
VERSION A37272.1 GI:2294369
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1585)
AUTHORS Vile,R.G. and Hart,I.R.
TITLE TUMOUR THERAPY
JOURNAL Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
FEATURES
source Location/Qualifiers
1. .1585
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
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Search completed: September 3, 2005, 01:14:21
Job time : 784.946 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 18:45:43 ; Search time 131.925 Seconds
(without alignments)
1929.494 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	43	AAZ99817	Aaz99817 Cis-actin
2	43	100.0	50	AAZ99815	Aaz99815 Sequence
3	43	100.0	104	AAZ99816	Aaz99816 Cis-actin
4	43	100.0	787	AAZ20979	Aaz20979 Human TNF
5	43	100.0	792	ADR12297	Adrl2297 Human tum
6	43	100.0	815	AAZ70075	Aan70075 Human ant
7	43	100.0	817	AAQ04340	Aaq04340 THP-1. 3/
8	43	100.0	818	AAZ91035	Aan91035 XhoI - Ps
9	43	100.0	1200	AAZ70072	Aan70072 Human ant
10	43	100.0	1200	AAZ90969	Aan90969 Part of g
11	43	100.0	1275	AAZ60558	Aan60558 Sequence
12	43	100.0	1279	ADE25716	Ade25716 Human CDN
13	43	100.0	1323	AAZ60363	Aan60363 Sequence
14	43	100.0	1324	AAZ34963	Aaa34963 Human ade
15	43	100.0	1324	AAZ21085	Aaf21085 Human low
16	43	100.0	1324	ABZ96779	Abz96779 Human nuc
17	43	100.0	1324	ABD20628	Abd20628 Human pul
18	43	100.0	1560	AAZ80219	Aan80219 Sequence
19	43	100.0	1581	ADQ83817	Adq83817 Human tum
20	43	100.0	1585	AAZ60527	Aan60527 Sequence

21	43	100.0	1585	1	AAN60557	Aan60557 Sequence
22	43	100.0	1585	8	ACA64836	ACA64836 Human TNF
23	43	100.0	1585	10	ADF76346	Adf76346 Novel hum
24	43	100.0	1585	11	ADI32003	Adi32003 Human CDN
25	43	100.0	1585	12	ADO19587	Adol19587 Human PRO
26	43	100.0	1585	13	ADR24640	Adr24640 Breast ca
27	43	100.0	1585	13	ADP54654	Adp54654 Human PRO
28	43	100.0	1606	1	AAZ60446	Aan60446 Sequence
29	43	100.0	1606	2	AAT15424	Aat15424 Human tum
30	43	100.0	1643	1	AAZ71307	Aan71307 Sequence
31	43	100.0	1643	2	AAT31021	Aat31021 Human tum
32	43	100.0	1643	6	ABK13195	Abk13195 Human tum
33	43	100.0	1643	8	AAL53712	Aal53712 Tumour ne
34	43	100.0	1643	8	AAD49644	Aad49644 Human tum
35	43	100.0	1643	10	ADC35185	Adc35185 Human CDN
36	43	100.0	1643	10	AAD63904	Aad63904 Human TNF
37	43	100.0	1643	10	ACC57575	Acc57575 Polynucle
38	43	100.0	1643	13	ADR26040	Adr26040 Breast ca
39	43	100.0	1650	8	ACF64375	Acf64375 Human TNF
40	43	100.0	1666	10	ADE25664	Ade25664 Human CDN
41	43	100.0	1669	13	ADS88038	Ads88038 Tumour tr
42	43	100.0	1669	13	ADT08160	Adt08160 Human tum
43	43	100.0	2270	2	AAZ20983	Aaz20983 Chimeric
44	43	100.0	2570	2	AAZ20984	Aaz20984 Chimeric
45	43	100.0	3634	2	AAV39005	Aav39005 TNF-alpha

ALIGNMENTS

RESULT 1
AAZ99817
ID AAZ99817 standard; RNA; 43 BP.
XX

AC AAZ99817;

DT 12-JUL-2000 (first entry)

DE Cis-acting nucleotide sequence derived from human TNF-alpha.

XX Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

OS Homo sapiens.

XX WO2000014255-A1.

PD 16-MAR-2000.

PF 06-SEP-1999; 99WO-IL000483.

XX 07-SEP-1998; 98IL-00126112.

PR 26-OCT-1998; 98IL-00126757.

XX (YISS) YISSUM RES & DEV CO.

PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

XX WPI; 2000-257000/22.

PT Regulation of gene expression by mRNA splicing is carried out using a cis
-acting nucleotide sequence controlled by phosphorylation of the alpha-
subunit of eukaryotic initiation factor 2.

XX Claim 5; Page 15; 75pp; English.

PS The specification describes a cis-acting nucleotide sequence which is
capable of removing introns from a precursor transcript encoded by a gene
which harbours at least one cis-acting nucleotide sequence. This removal
is effected during the production of mRNA of the gene, and depends on
activation of a trans-acting factor which is an RNA-activated protein
kinase capable of phosphorylating the alpha-subunit of eukaryotic

CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can be
CC used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention
XX
SQ Sequence 43 BP; 10 A; 13 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||
Db 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

RESULT 2
AAZ99815
ID AAZ99815 standard; RNA; 50 BP.
AC AAZ99815;
XX
DT 12-JUL-2000 (first entry)
DE
DE Sequence of the stem loop of tumour necrosis factor-alpha gene.
XX

KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX

OS Homo sapiens.
XX
XX WO200014255-A1.
XX
PD 16-MAR-2000.
XX

PF 06-SEP-1999; 99WO-IL0000483.
XX
XX 07-SEP-1998; 98IL-00126112.
PR 26-OCT-1998; 98IL-00126757.
XX
XX (YISS) YISSUM RES & DEV CO.
PA

PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
XX WPI; 2000-257000/22.
DR

XX Regulation of gene expression by mRNA splicing is carried out using a cis
PT -acting nucleotide sequence controlled by phosphorylation of the alpha-
PT subunit of eukaryotic initiation factor 2.
XX

PS Example 7; Fig 5B; 75pp; English.
XX

CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a gene
CC which harbours at least one cis-acting nucleotide sequence. This removal
CC is effected during the production of mRNA of the gene, and depends on
CC activation of a trans-acting factor which is an RNA-activated protein
CC kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can be
CC used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant

CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a fragment of the 3'UTR of human TNF-alpha
XX
SQ Sequence 50 BP; 12 A; 15 C; 12 G; 0 T; 11 U; 0 Other;
Query Match 100.0%; Score 43; DB 3; Length 50;
Best Local Similarity 79.1%; Pred. No. 4.4e-07;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 UCAAAACUGGGGCCUCCAGAACUCACUGGGGCCUACAGCUUUGA 47

RESULT 3
AAZ99816
ID AAZ99816 standard; RNA; 104 BP.
XX
AC AAZ99816;
XX
DT 12-JUL-2000 (first entry)
XX

DE Cis-acting nucleotide sequence derived from human TNF-alpha.
XX
XX Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.
XX
OS Homo sapiens.
XX
XX WO200014255-A1.
XX

PD 16-MAR-2000.
XX
XX 06-SEP-1999; 99WO-IL0000483.
PF
XX
PR 07-SEP-1998; 98IL-00126112.
PR 26-OCT-1998; 98IL-00126757.
XX
XX (YISS) YISSUM RES & DEV CO.
XX

PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;
XX
XX WPI; 2000-257000/22.
DR

XX Regulation of gene expression by mRNA splicing is carried out using a cis
PT -acting nucleotide sequence controlled by phosphorylation of the alpha-
PT subunit of eukaryotic initiation factor 2.
XX
XX Claim 4; Page 15; 75pp; English.
PS
XX

CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a gene
CC which harbours at least one cis-acting nucleotide sequence. This removal
CC is effected during the production of mRNA of the gene, and depends on
CC activation of a trans-acting factor which is an RNA-activated protein
CC kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders
CC splicing of precursor transcripts encoded by that gene sensitive to the
CC level of RNA-activated protein kinase (PKR) activity. The sequence can be
CC used to transform host cells to regulate gene expression at the mRNA
CC splicing level, for gene therapy, and to produce a recombinant
CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
CC protein) or industrially or agriculturally applicable protein. The
CC present sequence represents a cis-acting nucleotide sequence of the
CC invention
XX
SQ Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 3; Length 104;

Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47

RESULT 4

AAZ20979
ID AAZ20979 standard; DNA; 787 BP.
XX
AC AAZ20979;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human TNFalpha 3'UTR.
XX
KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus; diabetes;
KW ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
PN WO9943840-A1.
XX
PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99WO-US000637.
XX
PR 27-FEB-1998; 98US-0076316P.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Tataka RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX
PT A chimeric polynucleotide consisting of a tissue necrosis factor (TNF)
PT promoter and an apoptosis-inducing Granzyme B polynucleotide.
XX
PS Example 1; Page 60-61; 71pp; English.
XX

This sequence represents a human TNFalpha (tumour necrosis factor alpha) 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were constructed comprising at least one TNFalpha promoter enhancer region (AAZ20975-Z20978), a TNFalpha promoter (AAZ20972-Z20974), a DNA encoding the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha 3'UTR sequence. TNFalpha is one of a number of cytokines produced by inflammatory cells. Upregulation and/or dysregulation of cytokines in inflamed tissue may be directly or indirectly responsible for exacerbation of chronic inflammatory diseases. Introduction of the chimeric nucleotide to activated inflammatory cells causes them to undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide may be useful for treating inflammatory disorders such as multiple sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus host disease, lupus erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis, and in particular, rheumatoid arthritis. The use of such chimeric nucleotides offers simpler and cheaper long-term relief, in comparison with existing conventional pharmaceutical and invasive surgery methods

Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 5
ADR12297
XX ADR12297 standard; DNA; 792 BP.
AC ADR12297;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human tumour necrosis factor alpha 3'-untranslated region DNA.
XX
KW ss; cytostatic; VEGF modulator; angiogenesis inhibitor;
KW UTR-dependent expression; vascular endothelial growth factor;
KW untranslated region; cancer; angiogenesis.
XX
OS Homo sapiens.
XX
PN WO2004065561-A2.
XX
PD 05-AUG-2004.
XX
PF 21-JAN-2004; 2004WO-US001643.
XX
PR 21-JAN-2003; 2003US-0441637P.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
XX
PI Cao L, Trifillis P;
XX
DR WPI; 2004-571681/55.
XX

Identifying modulators of untranslated region-dependent expression of a VEGF gene, useful for treating cancer, comprises contacting a compound with a cell or translation mixture containing a reporter gene linked to a VEGF gene UTR.

Example; SEQ ID NO 6; 251pp; English.

A method of identifying (M1) a compound that modulates untranslated region-dependent expression of a vascular endothelial growth factor (VEGF) gene comprises contacting a member of a library of compounds with a cell or cell-free translation mixture containing a reporter gene operably linked to an untranslated region (UTR) of the VEGF gene, and detecting expression of the reporter gene. A compound is identified as a modulator if the level of expression of the reporter gene in the presence of the compound is altered as compared to that in the absence of the compound or in the presence of a control. Compounds identified by M1 are useful for treating, preventing or ameliorating cancer or its symptoms, and/or for inhibiting angiogenesis. This sequence corresponds to a therapeutic untranslated region used in the invention.

Sequence 792 BP; 192 A; 203 C; 172 G; 225 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 13; Length 792;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 223 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 265

RESULT 6

AAN70075
ID AAN70075 standard; DNA; 815 BP.
XX
AC AAN70075;
XX
DT 25-MAR-2003 (revised)
DT 20-JAN-1991 (first entry)
XX
DE Human anti-tumor polypeptide Xho-PstI fragment.
XX

KW Anti-tumor; cancer; cytotoxic; ss.
XX
OS Homo sapiens.
XX
PN EP247906-A.
XX
PD 02-DEC-1987.
XX
PF 04-FEB-1987; 87EP-00400261.
XX
PR 04-FEB-1986; 86JP-00021302.
PR 07-FEB-1986; 86JP-00024220.
PR 17-JUL-1986; 86JP-00169522.
XX
PA (MIZU/) MIZUNO D.
XX
PI Mizuno D, Soma GI;
PI
DR WPI; 1987-336540/48.
XX
PT Anti-tumour polypeptide(s) - prepd. using recombinant DNA prepd. from
PT genomic DNA of human acute leukaemia cell thp-1.
XX
PS Disclosure; Fig 7; 63pp; English.
XX
CC The sequence is an Xho-PstI fragment of an anti-tumor protein. The
CC polypeptide is cytotoxic to human tumor cells but not to normal cells.
CC They are also cytotoxic to primary cell cultures obtained from metastasis
CC lesions of patients suffering from striated muscle tumors. They are also
CC resistant to all chemotherapeutic agents. See also AAN70073-74, AAP70077-
CC 78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 1; Length 815;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758

RESULT 7
AAQ04340
ID AAQ04340 standard; DNA; 817 BP.
XX
AC AAQ04340;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1990 (first entry)
XX
DE THP-1.
XX
KW Acute leukaemia cell; THP-1; anti-tumour agent; ss.
XX
OS Homo sapiens.
PN JP02088598-A.
XX
PD 28-MAR-1990.
XX
PF 22-SEP-1988; 88JP-00239154.
XX
PR 22-SEP-1988; 88JP-00239154.
XX
PA (SOMA/) SOMA G.
XX
DR WPI; 1990-143138/19.
XX
PT Intrinsic TNF prodn. derivation agents - contain primer and trigger, at
PT least one of which has TNF activity.
XX

PS Disclosure; Page ?; 26pp; Japanese.
XX
CC Used in the prodn. of TNF prodn. agents. (Updated on 25-MAR-2003 to
CC correct PD field.)
XX
SQ Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 716 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 758

RESULT 8
AAN91035
ID AAN91035 standard; DNA; 818 BP.
XX
AC AAN91035;
XX
DT 27-AUG-2003 (revised)
DT 11-MAR-1990 (first entry)
XX
DE XhoI - PstI section of gene for anti-cancer peptide.
XX
KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX
OS THP 1 cells.
XX
PN JP01095784-A.
XX
PD 13-APR-1989.
XX
PF 06-OCT-1987; 87JP-00252174.
XX
PR 06-OCT-1987; 87JP-00252174.
XX
PA (SENG/) SEN G.
XX
DR WPI; 1989-154899/21.
XX
PT Novel DNA, plasmid and polypeptide(s) - useful as anticarcinogenic
PT agents.
XX
PS Fig 3; Page ?; 17pp; Japanese.
XX
CC Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA
CC from THP-1 cells. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 1; Length 818;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 717 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 759

RESULT 9
AAN70072
ID AAN70072 standard; DNA; 1200 BP.
XX
AC AAN70072;
XX
DT 25-MAR-2003 (revised)
DT 20-JAN-1991 (first entry)
XX
DE Human anti-tumor polypeptide.
XX

KW Anti-tumor; cancer; cytotoxic; ss.
XX Homo sapiens.
OS
XX EP247906-A.
PN
XX
PD 02-DEC-1987.
XX
XX 04-FEB-1987; 87EP-00400261.
PF
XX
PR 04-FEB-1986; 86JP-00021302.
PR 07-FEB-1986; 86JP-00024220.
PR 17-JUL-1986; 86JP-00169522.
XX
PA (MIZU/) MIZUNO D.
XX
PI Mizuno D, Soma GI;
XX
DR WPI; 1987-336540/48.
XX
PT Anti-tumour polypeptide(s) - prepd. using recombinant DNA prepd. from
PT genomic DNA of human acute leukaemia cell thp-1.
XX
PS Disclosure; Fig 4; 63pp; English.
XX
CC The polypeptide is cytotoxic to human tumor cells but not to normal
CC cells. They are also cytotoxic to primary cell cultures obtained from
CC metastasis lesions of patients suffering from striated muscle tumors.
CC They are also resistant to all chemotherapeutic agents. See also AAN70073
CC -75, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 1; Length 1200;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
DB 1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141
RESULT 10
AAN90969
ID AAN90969 standard; DNA; 1200 BP.
XX
AC AAN90969;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 11-MAR-1990 (first entry)
XX
DE Part of gene for anti-cancer peptide.
XX
KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX
OS THP 1 cells.
XX
PN JP01095784-A.
XX
PD 13-APR-1989.
XX
PF 06-OCT-1987; 87JP-00252174.
XX
PR 06-OCT-1987; 87JP-00252174.
XX
PA (SENG/) SEN G.
XX
DR WPI; 1989-154899/21.
XX
PT Novel DNA, plasmid and polypeptide(s) - useful as anticarcinogenic
PT agents.

XX Fig 2; Page ?; 17pp; Japanese.
PS
XX Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1
CC cells. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-
CC 2003 to correct OS field.)
XX
SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 1; Length 1200;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
DB 1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141
RESULT 11
AAN60558
ID AAN60558 standard; DNA; 1275 BP.
XX
AC AAN60558;
XX
DT 28-JUL-1991 (first entry)
XX
DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser
DE 69 in pAW731.
XX
KW Antitumour; anticancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..474
FT /*tag= a
XX
PN WO8604606-A.
XX
PD 14-AUG-1986.
XX
PF 03-FEB-1986; 86WO-US000236.
XX
PR 07-FEB-1985; 85US-00698939.
XX
PA (CETU) CETUS CORP.
XX
PI Mark DF, Lin LS, Lu SDY, Wang AM;
XX
DR WPI; 1986-225458/34.
DR P-PSDB; AAP60656.
XX
PT New synthetic muteins of human tumour necrosis factor protein - are obtd.
PT by direct mutagenesis and retain antitumour activity.
XX
PS Disclosure; Fig 3a; 47pp; English.
XX
CC The sequence encoding TNF produced by the promyelocytic leukemia cell
CC line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see
CC AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
CC sequence appears to be involved in disulphide linkages. The patentors
CC claim a novel synthetic mutein of a biologically active hTNF protein,
CC having at least one cysteine residue free from a disulphide link and non-
CC essential to the activity and having at least one of the cysteine
CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
CC claimed
XX
SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 1; Length 1275;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 739

RESULT 12
ADE25716
ID ADE25716 standard; cDNA; 1279 BP.
AC ADE25716;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cDNA differentially expressed in foam cells #120.
XX
KW Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;
KW cardiovascular disease; atherosclerosis.
OS Homo sapiens.
XX
PN US2003194721-A1.
XX
PD 16-OCT-2003.
XX
PF 18-SEP-2002; 2002US-00247671.
XX
PR 19-SEP-2001; 2001US-0323784P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Mikita T, Shiffman D, Porter JG, Kaser MR;
XX
DR WPI; 2003-875398/81.
DR P-PSDB; ADE25778.
XX
PT Combination containing several polynucleotide that are differentially
PT expressed in foam cells and complements of the polynucleotides, useful
PT for diagnosing cardiovascular disease or atherosclerosis.
XX
PS Claim 1; SEQ ID NO 120; 37pp; English.
XX

CC The invention relates to a combination comprising several polynucleotides
CC having any one of 127 sequences (S1) such as the sequence of human
CC calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4
CC hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit
CC mRNA, etc., and their complements. The cDNAs are differentially expressed
CC in LPS (lipopolysaccharide)-treated foam cells. Also included are
CC obtaining an extended or full length gene from a library of nucleic acid
CC sequences, an expression vector containing the nucleic acids, a host cell
CC containing the vector, a purified polypeptide appearing as ADE25750 and
CC ADE25751, producing a protein by culturing the host cell, and a
CC composition comprising a purified antibody that specifically binds to the
CC proteins. The foam cell-expressed nucleic acids are useful for a high
CC throughput detection of differential expression of one or more
CC polynucleotides in a sample. The sample is from a subject with
CC atherosclerosis and comparison with a standard defines early, mid or late
CC stages of the disorder. The foam cell-expressed nucleic acids are useful
CC for high throughput screening of a library of molecules or compounds to
CC identify a ligand which binds a polynucleotide. The library is chosen
CC from DNA molecules, peptides, proteins and RNA molecules. The protein is
CC useful for a high throughput screening of library of molecules or
CC compounds to identify at least one ligand which specifically binds a
CC protein, for purifying a ligand from a sample for making a antibody. The
CC foam cell-expressed nucleic acids are useful for diagnosing
CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful
CC as elements on a microarray which can be used for detecting related
CC polynucleotide in a sample, diagnosing cardiovascular disease,
CC atherosclerosis. The present sequence represents a cDNA whose expression
CC is upregulated in LPS treated foam cells.

SQ Sequence 1279 BP; 293 A; 415 C; 323 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 10; Length 1279;

Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1081 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1123

RESULT 13
AAN60363
ID AAN60363 standard; DNA; 1323 BP.
XX
AC AAN60363;
XX
DT 19-JUN-1991 (first entry)
XX
DE Sequence encoding human tumour necrosis factor.
XX
KW hTNF; tumour; cancer; interferon; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..534
FT /*tag= a
FT sig_peptide 1..60
FT /*tag= b
FT /label= Secretory leader peptide
FT mat_peptide 61..534
FT /*tag= c

PN EP168214-A.

XX
PD 15-JAN-1986.

XX
PF 03-JUL-1985; 85EP-00304758.

XX
PR 05-JUL-1984; 84US-00627959.

PR 05-JUL-1984; 84US-00628059.

PR 05-JUL-1984; 84US-00628060.

PR 03-DEC-1984; 84US-00677156.

PR 03-DEC-1984; 84US-00677257.

PR 03-DEC-1984; 84US-00677267.

PR 03-DEC-1984; 84US-00677454.

XX (GETH) GENENTECH INC.

XX Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;

PI WPI; 1986-015483/03.

XX P-PSDB; AAP60417.

DR Pure tumour necrosis factor and mutant forms - new DNA coding sequences

XX and transformed cells.

XX Claim 20; Fig 10; 90pp; English.

CC Sequence encodes the pure human tumour necrosis factor, mutants of which
CC are covered by the claims. TNF and mutants are useful in treating
CC tumours, especially in tandem with interferon. The encoding sequence may
CC be used to create plasmid pTRpXAPTNF, allowing transformation of an
CC E.coli host for the expression of TNF

XX
SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 1; Length 1323;

Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

Db 754 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 796

CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention

XX

SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 3; Length 1324;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797

Search completed: September 3, 2005, 00:29:35
Job time : 132.925 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 23:36:03 ; Search time 983.15 Seconds
(without alignments)
1664.816 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	43	100.0	474	5	BX118951	BX118951 BX118951
C 3	43	100.0	630	6	CB528492	CB528492 UI-H-FT2-
C 4	43	100.0	645	6	CD370363	CD370363 UI-H-FT1-
C 5	43	100.0	684	6	CA307429	CA307429 UI-H-FT1-
C 6	43	100.0	688	6	CD367676	CD367676 UI-H-FT1-
C 7	43	100.0	696	6	CA307225	CA307225 UI-H-FT1-
C 8	43	100.0	699	6	CD364761	CD364761 UI-H-FT2-
C 9	43	100.0	703	6	CD368142	CD368142 UI-H-FT1-
C 10	43	100.0	713	6	CA308256	CA308256 UI-H-FT1-
C 11	43	100.0	719	6	CB528694	CB528694 UI-H-FT2-
C 12	43	100.0	722	5	BQ007008	BQ007008 UI-H-E11-
C 13	43	100.0	722	6	CA307062	CA307062 UI-H-FT1-
C 14	43	100.0	722	6	CD364988	CD364988 UI-H-FT2-
C 15	43	100.0	723	6	CA308777	CA308777 UI-H-FT1-
C 16	43	100.0	723	6	CD368116	CD368116 UI-H-FT1-
C 17	43	100.0	724	6	CA309711	CA309711 UI-H-FT1-
C 18	43	100.0	726	6	CA310368	CA310368 UI-H-FT1-
C 19	43	100.0	726	6	CD368929	CD368929 UI-H-FT1-
C 20	43	100.0	742	6	CA309509	CA309509 UI-H-FT1-
C 21	43	100.0	744	6	CD366187	CD366187 UI-H-FT1-
C 22	43	100.0	748	6	CA306559	CA306559 UI-H-FT1-
C 23	43	100.0	755	6	CD240146	CD240146 DTL3P2G5
C 24	43	100.0	1068	1	AL543083	AL543083 AL543083

C 25	42	97.7	693	6	CD367625	CD367625 UI-H-FT1-
C 26	41.4	96.3	672	6	CD367664	CD367664 UI-H-FT1-
C 27	41.4	96.3	713	6	CA309664	CA309664 UI-H-FT1-
C 28	41.4	96.3	718	6	CD367794	CD367794 UI-H-FT1-
C 29	35.2	81.9	581	1	AI242177	AI242177 qh81g08.x
C 30	33.6	78.1	564	1	AA699697	AA699697 z178f12.8
C 31	28	65.1	561	4	BG232086	BG232086 naf332e06.
C 32	27.8	64.7	792	7	CK777347	CK777347 9643375 MA
C 33	25	58.1	1011	1	AL575811	AL575811 AL575811
C 34	24.8	57.7	431	8	AQ459761	AQ459761 HS_5125_A
C 35	24.6	57.2	608	6	CB426950	CB426950 602494 MA
C 36	24	55.8	594	7	N26123	N26123 yx90h08.s1
C 37	23.8	55.3	163	2	BF737938	BF737938 CM2-KT003
C 38	23.8	55.3	363	5	BY014887	BY014887 BY014887
C 39	23.6	54.9	172	2	BF855413	BF855413 RC4-FN020
C 40	23.6	54.9	545	1	AU260483	AU260483 AU260483
C 41	23.6	54.9	631	9	CE567682	CE567682 tigr-g88-
C 42	23.4	54.4	434	6	CB759234	CB759234 AMGNNUC:N
C 43	23.4	54.4	492	5	BY243201	BY243201 BY243201
C 44	23.4	54.4	763	5	BQ445871	BQ445871 UI-H-EU1-
C 45	23.4	54.4	2686	3	AK077502	Mus muscu

ALIGNMENTS

RESULT 1
T29839
LOCUS T29839 248 bp mRNA linear EST 06-SEP-1995
DEFINITION EST97164 Human Testis Homo sapiens cDNA 5' end similar to tumor necrosis factor, alpha (HT:1190), mRNA sequence.
ACCESSION T29839
VERSION T29839.1 GI:611937
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 248)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., HinkleJr,P.S., Kelley,J.M., Klimk,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegriano,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)
JOURNAL PUBMED 96026280
MEDLINE 7566098
COMMENT Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
Location/Qualifiers 1. .248
FEATURES source

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										0;	

of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 630;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 499 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 457

RESULT 4
CD370363/c

LOCUS
DEFINITION
UI-H-FT1-bkb-n-03-0-UI.s1 NCI_CGAP_FTI Homo sapiens cDNA clone
UI-H-FT1-bkb-n-03-0-UI 3', mRNA sequence.

ACCESSION
CD370363
VERSION
GI:31154453
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 645)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 294-368, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
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/dev_stage="Adult"
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/clone_lib="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3

hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 645;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 588 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 546

RESULT 5
CA307429/c

LOCUS
DEFINITION
UI-H-FT1-bic-i-01-0-UI.s1 NCI_CGAP_FTI Homo sapiens cDNA clone
UI-H-FT1-bic-i-01-0-UI 3', mRNA sequence.

ACCESSION
CA307429
VERSION
GI:24470483
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 684)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1. .684
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bic-i-01-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FTI"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of

the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Staph aureus moi 10, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 684;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

RESULT 6

CD367676/c
LOCUS
DEFINITION UI-H-FT1-bjr-1-14-0-UI.s1 mRNA linear EST 05-AUG-2004
UI-H-FT1-bjr-1-14-0-UI 3', mRNA sequence.

ACCESSION CD367676
VERSION CD367676.1 GI:31151766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 688)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 69-143, >(TAA)n#Simple_repeat
Seg primer: M13 FORWARD
POLYA=Yes.

FEATURES

source
1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjr-1-14-0-UI"
/tissue_type="Alveolar Macrophage"

/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Klebsiella moi 10, 24 hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 688;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 363 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 321

RESULT 7

CA307225/c
LOCUS
DEFINITION UI-H-FT1-bhu-n-04-0-UI.s1 mRNA linear EST 05-AUG-2004
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.

ACCESSION CA307225
VERSION CA307225.1 GI:24470279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 696)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu

The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..696
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-n-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The tissue tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548

RESULT 8
CD364761/c
LOCUS
DEFINITION
UI-H-FT2-bjm-j-11-0-UI.s1 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.
CD364761
ACCESSION
CD364761.1 GI:31148851
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 699)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
JOURNAL
COMMENT

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..699
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjm-j-11-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP FT2 is a substracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was substracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 699;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548

RESULT 9
CD368142/c
LOCUS
DEFINITION
UI-H-FT1-bjv-e-20-0-UI.s1 NCI CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.
CD368142
ACCESSION
CD368142.1 GI:31152232
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM

CD368142
703 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bjv-e-20-0-UI.s1 NCI CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.
CD368142
ACCESSION
CD368142.1 GI:31152232
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 703)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA sequence: 298-372, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..703
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bjv-e-20-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ft1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 703;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 592 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 550
|||||

RESULT 10
CA308256/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CA308256 713 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bhy-e-14-0-UI.s1 NCI_CGAP_Ft1 Homo sapiens cDNA clone
UI-H-FT1-bhy-e-14-0-UI 3', mRNA sequence.
CA308256
CA308256.1 GI:24471310
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..713
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-e-14-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ft1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1

Query Match 100.0%; Score 43; DB 5; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

RESULT 13
CA307062/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CA307062 722 bp mRNA linear EST 05-AUG-2004
UI-H-FT1-bhu-o-04-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bhu-o-04-0-UI 3', mRNA sequence.
CA307062
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 295-369, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..722
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhu-o-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_FT1 is a normalized cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
hours; wt adenovirus + LPS 24 hours. The library was
normalized according to Bonaldo, Lennon and Soares, Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,

digested with Not I, and cloned directionally into
pT7T3-Pac vector. The oligonucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 589 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 547

RESULT 14
CD364988/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CD364988 722 bp mRNA linear EST 05-AUG-2004
UI-H-FT2-bjn-c-04-0-UI.s1 NCI_CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.
CD364988
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 722)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjn-c-04-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_FT2 is a subtracted cDNA library constructed from
a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella

moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 722;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

RESULT 15
CA308777/c

LOCUS CA308777 723 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT1-bhy-b-23-0-UI.s1 NCI CGAP_Ft1 Homo sapiens cDNA clone
UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.

ACCESSION CA308777
VERSION CA308777.1 GI:24471831
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 723)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source Location/Qualifiers
1..723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Ft1"
/note="Organ: Lung; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Ft1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different

conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 100.0%; Score 43; DB 6; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 549

Search completed: September 3, 2005, 02:11:42
Job time : 985.15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 13:14:57 ; Search time 175.51 Seconds
(without alignments)
400.888 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length		
1	43	100.0	787	4 US-09-032-297A-13	Sequence 13, Appl
2	43	100.0	787	4 US-09-229-151C-7	Sequence 7, Appli
3	43	100.0	1585	4 US-09-023-655-1329	Sequence 1329, Ap
4	43	100.0	1587	4 US-09-949-016-5156	Sequence 5156, Ap
5	43	100.0	1643	3 US-08-880-342-36	Sequence 36, Appl
6	43	100.0	1643	3 US-09-505-250-4	Sequence 4, Appli
7	43	100.0	2270	4 US-09-229-151C-13	Sequence 13, Appl
8	43	100.0	2570	4 US-09-229-151C-14	Sequence 14, Appl
9	43	100.0	3634	3 US-09-166-186-1	Sequence 1, Appli
10	43	100.0	3634	3 US-09-313-932-1	Sequence 1, Appli
11	43	100.0	3634	3 US-09-109-663-34	Sequence 34, Appl
12	43	100.0	6682	4 US-09-949-016-16898	Sequence 16898, A
13	43	100.0	10728	4 US-09-376-774-5	Sequence 5, Appli
14	23	53.5	11752	4 US-09-949-016-11756	Sequence 11756, A
15	23	53.5	11865	4 US-09-949-016-15297	Sequence 15297, A
16	23	53.5	11865	4 US-09-949-016-15298	Sequence 15298, A
17	23	53.5	33753	4 US-09-949-016-15741	Sequence 15741, A
18	23	53.5	33756	4 US-09-949-016-12006	Sequence 12006, A
19	21.4	49.8	601	4 US-09-949-016-137730	Sequence 137730,
20	21.4	49.8	601	4 US-09-949-016-137731	Sequence 137731,
21	21.4	49.8	1274	4 US-09-148-545-72	Sequence 72, Appl
22	21.4	49.8	1296	4 US-09-148-545-126	Sequence 126, App
23	21.4	49.8	24707	4 US-09-740-027-3	Sequence 3, Appli
24	21.4	49.8	24720	4 US-09-949-016-12341	Sequence 12341, A
25	21.4	49.8	24721	4 US-09-949-016-15610	Sequence 15610, A
26	21.4	49.8	43133	4 US-09-949-016-14911	Sequence 14911, A
27	21.4	49.8	99498	4 US-09-949-016-12621	Sequence 12621, A

28	21.4	49.8	146428	4 US-09-949-016-12620	Sequence 12620, A
29	21.4	49.8	146438	4 US-09-949-016-12081	Sequence 12081, A
30	21	48.8	771	5 PCT-US95-12987-1	Sequence 1, Appli
31	21	48.8	771	5 PCT-US95-12987-3	Sequence 3, Appli
32	21	48.8	771	5 PCT-US95-12987-5	Sequence 5, Appli
33	21	48.8	229354	4 US-09-705-400-64	Sequence 64, Appl
34	21	48.8	636591	4 US-09-949-016-11808	Sequence 11808, A
35	21	48.8	636591	4 US-09-949-016-13388	Sequence 13388, A
36	20.8	48.4	249	4 US-09-513-999C-2202	Sequence 2202, Ap
37	20.8	48.4	285	4 US-09-513-999C-1777	Sequence 1777, Ap
38	20.8	48.4	493	4 US-09-621-976-978	Sequence 978, App
39	20.8	48.4	509	4 US-09-621-976-2765	Sequence 2765, Ap
40	20.8	48.4	534	4 US-09-621-976-714	Sequence 714, App
41	20.8	48.4	601	4 US-09-949-016-51785	Sequence 51785, A
42	20.8	48.4	861	1 US-08-409-731A-1	Sequence 1, Appli
43	20.8	48.4	861	2 US-08-470-298B-1	Sequence 1, Appli
44	20.8	48.4	861	2 US-09-023-073A-1	Sequence 1, Appli
45	20.8	48.4	861	3 US-09-361-737-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION:
; APPLICANT: Revati J. Tatake, Steven D. Marlin and
; Randall W. Barton
; TITLE OF INVENTION: Self-Regulated Apoptosis of
; Inflammatory Cells by Gene Therapy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Boehringer Ingelheim Corporation
; STREET: 900 Ridgebury Road, P.O. Box 368
; CITY: Ridgefield
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06877-0368
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,297A
; FILING DATE: 27-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,266
; FILING DATE: 28-FEB-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert P. Raymond
; REGISTRATION NUMBER: 25089
; REFERENCE/DOCKET NUMBER: 9/121PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-791-6183
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: DNA
; FEATURE:
; NAME/KEY: TNfa 3' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-032-297A-13

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Best Local Similarity 100.0%; Pred. No. 5.2e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 2
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; Sequence 7, Application US/092229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

Query Match 100.0%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 3
US-09-023-655-1329
; Sequence 1329, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g339737
US-09-023-655-1329

Query Match 100.0%; Score 43; DB 4; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 4
US-09-949-016-5156
; Sequence 5156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5156
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5156

Query Match 100.0%; Score 43; DB 4; Length 1587;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1051

RESULT 5
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: TNF cDNA HSTNFR (EMBL Accession
INDIVIDUAL ISOLATE: #X01394)
FEATURE:
NAME/KEY: CDS
LOCATION: 153..851
US-08-880-342-36

Query Match 100.0%; Score 43; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 6
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:

NAME/KEY: CDS
LOCATION: (153)...(854)
US-09-505-250-4
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Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116
RESULT 7
US-09-229-151C-13
; Sequence 13, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 13
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR
US-09-229-151C-13

Query Match 100.0%; Score 43; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 1709 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1751

RESULT 8
US-09-229-151C-14
; Sequence 14, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 14
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR
US-09-229-151C-14

Query Match 100.0%; Score 43; DB 4; Length 2570;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 2009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2051
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RESULT 9
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
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; LOCATION: (1589)..(1634)
; FEATURE:
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; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
; TITLE: homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

Query Match 100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854
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RESULT 10
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes:
; TITLE: structure, homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match 100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

RESULT 11

US-09-109-663-34
; Sequence 34, Application US/09109663
; Patent No. 6277981
; GENERAL INFORMATION:
; APPLICANT: Tu, Guang-Chou
; APPLICANT: Israel, Yedy
; TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
; TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 9855-3U1
; CURRENT APPLICATION NUMBER: US/09/109,663
; CURRENT FILING DATE: 1998-07-03
; EARLIER APPLICATION NUMBER: 60/051,705
; EARLIER FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34

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Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854
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RESULT 12

US-09-949-016-16898
; Sequence 16898, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16898
; LENGTH: 6682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16898

Query Match 100.0%; Score 43; DB 4; Length 6682;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13

US-09-376-774-5/c
; Sequence 5, Application US/09376774

; Patent No. 6759236
; GENERAL INFORMATION:
; APPLICANT: Fung, Yuen Kai
; APPLICANT: Gomer, Charles
; APPLICANT: T'Ang, Anne
; TITLE OF INVENTION: Methods To Enhance And Confine Expression
; TITLE OF INVENTION: Of Genes
; FILE REFERENCE: D6087
; CURRENT APPLICATION NUMBER: US/09/376,774
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/096,947
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 10728
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: recombinant vector pDATH-TNF?
US-09-376-774-5

Query Match 100.0%; Score 43; DB 4; Length 10728;
Best Local Similarity 100.0%; Pred. No. 8.8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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RESULT 14

US-09-949-016-11756
; Sequence 11756, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11756
; LENGTH: 11752
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(11752)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11756

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Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCT 39
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RESULT 15

US-09-949-016-15297
; Sequence 15297, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15297
; LENGTH: 11865
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(11865)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15297

Query Match 53.5%; Score 23; DB 4; Length 11865;
Best Local Similarity 74.4%; Pred. No. 13;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Db 4740 TCCATTGGGGGTCCAGAGCCCACTGGGGCCTGCAGGT 4778

Search completed: September 2, 2005, 18:55:20
Job time : 177.51 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2005, 15:27:57 ; Search time 198.034 Seconds
(without alignments)
1421.994 Million cell updates/sec

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Perfect score: 43
Sequence: 1 tcaactggggcctccagaa.....actgggctacagctttga 43

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	43	9 US-09-801-371A-2	Sequence 2, Appli
2	43	100.0	43	9 US-09-801-371A-6	Sequence 6, Appli
3	43	100.0	50	9 US-09-801-371A-8	Sequence 8, Appli
4	43	100.0	81	9 US-09-801-371A-7	Sequence 7, Appli
5	43	100.0	104	9 US-09-801-371A-1	Sequence 1, Appli
6	43	100.0	104	9 US-09-801-371A-5	Sequence 5, Appli
7	43	100.0	787	18 US-10-356-308A-13	Sequence 13, Appli

8	43	100.0	798	21	US-10-895-393-9	Sequence 9, Appli
9	43	100.0	806	20	US-10-814-634A-5	Sequence 5, Appli
10	43	100.0	1279	16	US-10-247-671-120	Sequence 120, App
11	43	100.0	1585	17	US-10-172-118-501	Sequence 501, App
12	43	100.0	1585	18	US-10-342-887-501	Sequence 501, App
13	43	100.0	1585	18	US-10-641-643-1329	Sequence 1329, Ap
14	43	100.0	1585	20	US-10-370-715B-19	Sequence 19, Appli
15	43	100.0	1643	15	US-10-272-411-4	Sequence 4, Appli
16	43	100.0	1643	15	US-10-218-547-3	Sequence 3, Appli
17	43	100.0	1643	15	US-10-272-328A-4	Sequence 4, Appli
18	43	100.0	1643	16	US-10-310-793-9	Sequence 9, Appli
19	43	100.0	1643	17	US-10-172-118-1901	Sequence 1901, Ap
20	43	100.0	1643	18	US-10-342-887-1901	Sequence 1901, Ap
21	43	100.0	1643	20	US-10-475-024-6	Sequence 6, Appli
22	43	100.0	1643	21	US-10-929-182-1	Sequence 1, Appli
23	43	100.0	1643	22	US-10-475-026-6	Sequence 6, Appli
24	43	100.0	1666	16	US-10-247-671-68	Sequence 68, Appli
25	43	100.0	1669	20	US-10-799-345-17	Sequence 17, Appli
26	43	100.0	1669	20	US-10-688-845-74	Sequence 74, Appli
27	43	100.0	2088	9	US-09-973-850-1	Sequence 1, Appli
28	43	100.0	2088	9	US-09-973-850-2	Sequence 2, Appli
29	43	100.0	2088	9	US-09-973-850-3	Sequence 3, Appli
30	43	100.0	3634	10	US-09-824-322B-1	Sequence 1, Appli
31	43	100.0	3634	10	US-09-932-300-34	Sequence 34, Appli
32	43	100.0	3634	17	US-10-191-997-104	Sequence 104, App
33	43	100.0	3634	18	US-10-202-062-3	Sequence 3, Appli
34	43	100.0	3634	19	US-10-652-795-1	Sequence 1, Appli
35	43	100.0	3634	19	US-10-647-918-1	Sequence 1, Appli
36	43	100.0	3634	21	US-10-770-970-1	Sequence 1, Appli
37	43	100.0	3634	24	US-11-028-780-3	Sequence 3, Appli
38	43	100.0	4830	17	US-10-429-802-33	Sequence 33, Appli
39	43	100.0	4830	17	US-10-430-503-24	Sequence 24, Appli
40	43	100.0	14036	21	US-10-741-600-17806	Sequence 17806, A
41	43	100.0	14769	21	US-10-741-600-18012	Sequence 18012, A
42	43	100.0	22173	19	US-10-322-696-28	Sequence 28, Appli
43	35	81.4	418	9	US-09-796-692-6223	Sequence 6223, Ap
44	35	81.4	418	14	US-10-040-862-6223	Sequence 6223, Ap
45	35	81.4	418	17	US-10-057-475B-6223	Sequence 6223, Ap

ALIGNMENTS

RESULT 1
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2

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Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
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; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

Query Match      100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1

RESULT 3
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

Query Match      100.0%; Score 43; DB 9; Length 50;
Best Local Similarity 79.1%; Pred. No. 8e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      5 UCAAAACUGGGGCCUCCAGAAACUCACUGGGGCCUACAGCUUUGA 47

RESULT 4
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 81
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-7

Query Match      100.0%; Score 43; DB 9; Length 81;
Best Local Similarity 79.1%; Pred. No. 8e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      9 UCAAAACUGGGGCCUCCAGAAACUCACUGGGGCCUACAGCUUUGA 51

RESULT 5
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match      100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      5 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47

RESULT 6
US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1
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FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 104
TYPE: DNA
ORGANISM: Homo sapien
US-09-801-371A-5

Query Match 100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 100 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 58

RESULT 7
US-10-356-308A-13
Sequence 13, Application US/10356308A
Publication No. US20040039186A1
GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Marlin, Steven D.
APPLICANT: Barton, Randall Wilber
TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
FILE REFERENCE: 9/121-1-CIP1
CURRENT APPLICATION NUMBER: US/10/356,308A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 09/032,297
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: US 60/039,266
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 787
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: 1 to 787
OTHER INFORMATION: TNFa 3' untranslated region
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E., et al.
JOURNAL: Nucleic Acid Research
VOLUME: 13
PAGES: 6361-6373
DATE: 1985
US-10-356-308A-13

Query Match 100.0%; Score 43; DB 18; Length 787;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 8
US-10-895-393-9
Sequence 9, Application US/10895393
Publication No. US20050048549A1
GENERAL INFORMATION:
APPLICANT: CAO, Liangxian
APPLICANT: MEHTA, Anuradha
APPLICANT: NARYSHKIN, Nikolai A.
APPLICANT: PELLEGRINI, Matthew C.

APPLICANT: ROMFO, Charles M.
APPLICANT: TRIPILLIS, Panayiota
APPLICANT: TROTTA, Christopher R.
TITLE OF INVENTION: Methods and Agents for Screening for Compounds Capable of Modulating Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: 19025.012
CURRENT APPLICATION NUMBER: US/10/895,393
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: PCT/US04/01643
PRIOR FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/441,637
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 798
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-895-393-9

Query Match 100.0%; Score 43; DB 21; Length 798;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 220 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 262

RESULT 9
US-10-814-634A-5
Sequence 5, Application US/10814634A
Publication No. US20040231007A1
GENERAL INFORMATION:
APPLICANT: CHENEVAL, Dominique
APPLICANT: KASTELIC, Tania
APPLICANT: Novation Pharmaceuticals Inc.
TITLE OF INVENTION: Assay for Identifying Compounds Which Affect Stability of mRNA
FILE REFERENCE: 793-104CIP
CURRENT APPLICATION NUMBER: US/10/814,634A
CURRENT FILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: US 09/869,159
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: GB 9828709.7
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 806
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-814-634A-5

Query Match 100.0%; Score 43; DB 20; Length 806;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 231 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 273

RESULT 10
US-10-247-671-120
Sequence 120, Application US/10247671
Publication No. US20030194721A1
GENERAL INFORMATION:
APPLICANT: Mikita, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Porter, Gordon, J.

```
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 120
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
US-10-247-671-120
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Query Match      100.0%; Score 43; DB 16; Length 1279;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db      1081 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1123
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RESULT 11
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 000594
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501
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Query Match      100.0%; Score 43; DB 17; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db      1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049
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RESULT 12
US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
```

```
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-501
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```
Query Match      100.0%; Score 43; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db      1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049
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RESULT 13
US-10-641-643-1329
; Sequence 1329, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
;              Susan G. Stuart
;              Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;              GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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;
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g339737
; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329

Query Match          100.0%; Score 43; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 14
US-10-370-715B-19
; Sequence 19, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 19
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-19

Query Match          100.0%; Score 43; DB 20; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 15
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
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; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match          100.0%; Score 43; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

Search completed: September 3, 2005, 00:21:56
Job time : 198.034 secs
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